

Remarks

Claims 1-43, 72-75, 83-91, and 133-141 are pending. Claims 44-71, 76-82 and 92-132 have been withdrawn from consideration. Claims 1 and 84-86 have been amended to include the word “isolated” but this does not limit or change the scope of the claim as it was clear that the claims were limited to isolated nucleic acids as the two genes discussed in claim 1 are not on a single human chromosome as discussed below. This amendment was made to facilitate prosecution and later prosecution on this issue is reserved.

I. Rejection under 35 U.S.C. § 102

Applicant acknowledges and appreciates the withdrawal of the rejection of claims 1-4 under 35 U.S.C. § 102.

II. Rejection under 35 U.S.C. § 103(a)

Applicant acknowledges and appreciates the withdrawal of the rejection of claims 1-41, 72-75, 83-91 under 35 U.S.C. § 103.

III. Rejection under 35 U.S.C. § 101

Claims 1-43, 84-91, and 133-141 continue to be rejected under 35 U.S.C. § 101 for allegedly being directed to non-statutory subject matter. The Office Action argues that the claims read on a human comprising a nucleic acid, wherein the nucleic acid comprises a sequence encoding a HEX- α and a sequence encoding a HEX- β . The Examiner has pointed out that the definition of “composition” can be read broadly to encompass humans and has indicated that amending the claim to include “isolated” would alleviate this issue.

However, the fact that the claim is directed to a *composition* which could arguably include a human is irrelevant as the claims are directed to a composition comprising a single nucleic acid comprising both genes. Claim 1 is directed to a nucleic acid, “wherein the nucleic acid comprises a sequence encoding a HEX- α and a sequence encoding a HEX- β ”. Thus, the claims require that HEX- α and HEX- β be on a single nucleic acid. In a human, HEX- α and HEX- β are located on chromosomes 15 (see XM_037778) and 5 (see XM_032554), respectfully,

and in mouse on chromosome 9 (see NM_010421) and 13 (see NM_010422), respectfully. Thus, there is no single nucleic acid in humans (or mice) comprising sequences encoding both HEX- α and HEX- β . Claims 1-43, 84-91, and 133-141 are therefore directed to statutory subject matter, and the applicant respectfully requests the withdrawal of this rejection and allowance of claims 1-43, 84-91, and 133-141. However, in an effort to facilitate prosecution claims 1 and 84-86 have been amended to include “isolated.”

IV. Double Patenting

Claims 1-43, 72-75, and 83-86 are provisionally rejected under 35 U.S.C. § 101 for statutory type double patenting as allegedly claiming the same invention as that of claims 1-43, 72-75, and 83-86 of co-pending Application No. 10/978,927. This is a provisional rejection since the conflicting claims have not in fact been patented. Thus, the Applicant takes no action at this time. Once all other rejections have been removed, Applicant will likely file the appropriate Terminal Disclaimer.

V. Rejection under 35 U.S.C. § 112, first paragraph - Enablement

Claims 1-43, 72-75, 83-91, and 133-141 are rejected under 35 U.S.C. § 112, first paragraph, for allegedly failing to comply with the enablement requirement. The Examiner observes that the claims encompass the creation of functional HEXB-HEXA constructs using any sequence encoding a HEXA, any sequence encoding a HEXB, any IRES sequence, both orientations of bicistronic HEXA and HEXB, and any transposition system. The Examiner further notes that the claims encompass the delivery of HEXB-HEXA using any promoter (constitutive, inducible, or cell-specific), any vector (viral or non-viral), and with inducible systems *in vivo*. The Examiner does not believe that the specification enables a skilled person to make and use the invention commensurate with the scope of the claims.

The Examiner argues that the selection of the above identified components would require undue experimentation due to unpredictability. However, the Examiner appears to be basing this analysis on the presumption that the claimed compositions must be able to treat a disease. The

Examiner states that “[t]he claims, when read in view of the specification, have use in delivering HEX- α and HEX- β in order to ameliorate lysosomal disorders such as Tay-Sachs and Sandoffs diseases.” (Page 6, lines 4-6). While it is true that treating disease is a utility of some of the compositions, it is not the only identified use. For example, the specification provides for the use of the compositions as research tools (page 78, line 21). As the pending claims are directed to compositions, it is not appropriate for the Examiner to be applying a standard of enablement normally reserved for method of use claims. The assertion that the selection of promoters and vectors is unpredictable for the delivery of a nucleic acid to a subject for the treatment of a disease is not relevant to the pending claims. Thus, the Examiner has not made a *prima facia* case that the Applicant has not enabled the compositions or the method of making same. The following is a review of the enablement standard, followed by a discussion of the enablement of the HEXB-HEXA constructs and the method of delivery.

A. Enablement Standard

One determines undue experimentation not by analyzing a single factor, but rather by analyzing and weighing many factors. The legal standard set out in *In re Forman* 230 U.S.P.Q. 564, 547 (Bd. Pat. App. & Int. 1986) and elucidated in *In re Wands*, 858 F.2d 731, 737, 8 USPQ2d 1400 (Fed. Cir. 1988) sets forth the following factors for consideration: (1) The quantity of experimentation necessary (time and expense); (2) The amount of direction or guidance presented; (3) The presence or absence of working examples of the invention; (4) The nature of the invention; (5) The state of the prior art; (6) The relative skill of those in the art; (7) The predictability or unpredictability of the art; and (8) The breadth of the claims. It is not necessary that every enablement analysis consider all of the factors. *Amgen, inc. v. Chugai Pharmaceutical Co., LTD.*, 927 F.2d 1200, 1213 (Fed. Cir. 1991).

The fact that experimentation may be complex does not necessarily make it undue, if the art typically engages in such experimentation. *M.I.T. v. A.B. Fortia*, 774 F.2d 1104, 227 USPQ 428 (Fed. Cir. 1985). The test of enablement is not whether any experimentation is necessary,

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but whether, if experimentation is necessary, it is undue. *In re Angstadt*, 537 F.2d 498, 190 U.S.P.Q. 214 (CCPA 1976).

The facts underlying the decision of *In re Wands* illustrate well the concepts put forth in *MIT. A.B. Fortia* and *In re Angstadt*. The method claims at issue in *Wands* involved the use of an antibody wherein the “antibody is a monoclonal high affinity IgM antibody having a binding affinity constant for . . . [the antigen] of at least $10^9 M^{-1}$.” *In re Wands*, 858 F.2d at 734. This claim covers *any* monoclonal antibody, not just a specific monoclonal antibody, and the PTO argued that the Applicant failed to enable *all* monoclonal antibodies. *Id.* Briefly, the skilled artisan generates monoclonal antibodies by injecting an antigen into a host animal causing an immune reaction, isolating spleen cells, some of which produce the antibodies that bind the antigen, fusing the spleen cells with a cancerous myeloma cell producing a hybridoma, and then screening individual hybridomas to isolate those that produce antibodies that bind the antigen. *Id.* at 733-734. The PTO supported its non-enablement position by pointing out that 1) not all hybridomas produce antibodies that bind antigen, 2) not all hybridomas that bind antigen will bind with an affinity of $10^9 M^{-1}$, and 3) the Applicants own data indicated that a small percentage of hybridomas actually produced monoclonal antibodies which fell within the scope of the claims. *Id.* at 738-739. The court rejected these arguments by stating,

cell fusion [hybridoma technology] is a technique that is well known to those of skill in the monoclonal antibody art, . . . [t]here was a high level of skill in the art at the time when the application was filed, and all the methods needed to practice the invention were well known . . . [and] it seems unlikely that undue experimentation would be defined in terms of the number of hybridomas that were never screened, . . . [and since] Wands carried out his entire procedure three times, and was successful each time in making at least one antibody that satisfied all of the claim limitations . . . Wands evidence thus effectively rebuts the examiner’s challenge to the enablement of their disclosure.

Id. at 740. Furthermore, the *Wands* court made clear that the amount of and type of experimentation considered undue fluctuates for each type of art. *Id.* The quantity of

experimentation lacks relevance outside an assessment of what is “routine experimentation” in the art. *Id.* Thus, the huge amount of “experimentation” that the skilled artisan would have to perform to practice Wands’ invention: immunizing an animal, fusing lymphocytes from the immunized animals with myeloma cells to make hybridomas, cloning the hybridomas, and screening the hybridomas for the desired characteristics, *knowing that many hybridomas would not produce functional antibodies and not knowing which hybridomas would produce claimed antibody*, was not undue experimentation because it was routine experimentation in the art of monoclonal antibody production. *Id.* As discussed below, the present claims and corresponding enablement rejection closely parallel the situation presented in *Wands* since the art of producing the presently claimed nucleic acid constructs involves routine experimentation in the art of vector production even though it may seem complex.

B. What is enabled

The Examiner has acknowledged that the specification does in fact enable:

- 1) a tricistronic construct comprising the nucleic acid sequences SEQ ID NO:3 (HEXB), SEQ ID NO:5 (IRES), SEQ ID NO:1 (HEXA), and a lacZ, operably linked to CMV, rat nuclear enolase specific promoter (SEQ ID NO:69) or a rat pro-collagen 1 A1 promoter (SEQ ID NO:70, 71), wherein the construct is inserted into a non-viral mammalian expression vector system;
- 2) a tricistronic construct comprising the nucleic acid sequences SEQ ID NO:3 (HEXB), SEQ ID NO:5 (IRES), SEQ ID NO:1 (HEXA), and a lacZ, operably linked to CMV, rat nuclear enolase specific promoter (SEQ ID NO:69) or a rat pro-collagen 1 A1 promoter (SEQ ID NO:70, 71), wherein the construct is inserted into a FIV or HIV vector system;
- 3) a construct comprising a nucleic acid sequence comprising a transcription STOP site flanked by mammalian recombinase sites, the nucleic acid sequences SEQ ID NO:3 (HEXB), SEQ ID NO:5 (IRES), and SEQ ID NO:1 (HEXA), and a poly A tail, operably linked to CMV; and
- 4) a method of making the above constructs.

This indicates, appropriately so, that the claims are enabled for constructs actually reduced to practice and shown to work in the specification. This is consistent with the Examiner believing that testing or finding other constructs for the IRES sequence and/or the HEX sequences would constitute undue experimentation. This concern is addressed below.

C. Effective HEX constructs

The Examiner argues that the selection of other sequences encoding a HEXA, other sequences encoding a HEXB, other IRES sequence, or both orientations of bicistronic HEXA and HEXB, would require undue experimentation in order to create a functional construct. As stated above, the enablement standard, when properly applied to the composition claims, requires that one be able to make and use the HEXB-HEXA constructs without undue experimentation.

1. IRES

The Examiner cites LaPorte et al. (2000, *Journal of Virology*, 74:10827-10833) to argue the unpredictability of using different IRESes to initiate translation. In this report, the translation efficiencies of different IRESes varied from 3.4 to 93.6% relative to the original reporter vector, pIRF. The Examiner argues that the specification does not teach how to select IRESes such that enough HEXA and HEXB are produced to treat a disease. First, as stated above, the treatment of disease is not the correct standard for the present composition claims. No undue experimentation is required to produce a bicistronic construct that can produce both HEXA and HEXB, which according to the cited paper is possible even with the least efficient IRES. Second, even assuming the Examiner is correct and one must alleviate the disease, as discussed in the application, and consistent with the legal standard, any reduction in the disease state or symptoms would be sufficient for meeting the Examiner's overly high burden. Even under this unduly high burden, the publications cited by the Examiner would indicate that the claimed constructs would still work, as at least all constructs had 3.4% activity from the second gene. Thus, in the presently claimed material, as reported by LePorte, all of the constructs claimed by

the Applicants would have some activity, which is enough to meet even the Examiner's overly high standard.

In addition, the Examiner is directed to the standard and the facts set forth in Wands. Even if some constructs as claimed would work better than others, the ability to test these 1) is completely taught and within the four corners of the application, and 2) when this testing is predictable, as it is here, it is not considered undue, much like the screening of hundreds or thousands of antibodies to find the one that met the criteria claimed by Wands was not undue experimentation. The Examiner has indicated that the effect of the orientation and the variation of the HEX and IRES sequences must be "empirically determined" (Office Action at page 11). While Applicants maintain that this is not the case for the presently claimed constructs as they have been shown to work, assuming this to be the case, as discussed above and below "empirically determined" does not mean "undue experimentation." In fact, Wands stands for the very proposition that "empirical determination" in fact is explicitly not undue experimentation as Wands had to empirically determine each and every antibody which fell within the claims.

2. Bicistronic HEX Orientation

The Examiner cites Mizuguchi et al. (2000, Molecular Therapy, 1:376-382) and Hennecke et al. (2001, Nucleic Acids Research, 29:3327-3334) to argue that the lower amount of HEXB that would be produced by the IRES instead of the 5'cap would be enough to treat disease. The Examiner states:

"[w]hile the specification and the art teach that less gene product is made using an IRES, the specification does not teach an artisan that the lower amount of HexB, driven by the IRES, is enough to correct deficiencies in vitro and in vivo. The polycistronic constructs of the claimed invention need to be held to the standard that it treats a disorder as these are constructs that are used in gene therapy." (Page 9, lines 12-17).

As stated above, the treatment of disease is not the correct standard for the present composition claims. According to Mizuguchi et al. (2000), IRES-dependent second gene expression ranged from 6 to 100%, and in most cases was between 20 and 50%. Thus, no undue

experimentation is required to produce a bicistronic construct that can produce both HEXA and HEXB. In any event, the Examiner has applied this rejection to claims that have the orientation HEXB and HEXA which would address the Examiner's concerns, and so at least these claims should be allowed (claims 5, 7, and 84).

3. Bicistronic HEX Homology

The Examiner cites Hennecke et al. (2001, Nucleic Acids Research, 29:3327-3334) to argue the unpredictability of using homologues of HEX- α or HEX- β during IRES-mediated translation. Henneke et al. demonstrated that a 76.1% alteration of the Fluc nucleic acid sequence affected IRES-mediated translation of the second cistron. The Examiner is using an example of Fluz, which has less than 25% homology (76.1% of the coding nucleotide sequence was altered) to Fluc, to demonstrate the unpredictability of sequence modification on IRES-mediated translation. The Examiner uses this evidence to reject claim 12, wherein "the HEX- β has at least 70%, 75%, 80%, 85%, 90%, or 95% identity to the sequence set forth in SEQ ID NO:3" arguing that the variance will affect the translation ability of the second cistron. A set of variation having greater than 75% nonhomology cannot reasonably predict the outcome of claims having less than 30% nonhomology.

First, as discussed below, it is generally understood that a molecule with 70% or greater homology to a known sequence will have the essential physical properties of the identified structure. Evidence of divergence by a gene with only 25% homology is poor evidence of what a molecule with greater than 70% homology would do.

Second, as stated above, the treatment of disease is not the correct standard for the present composition claims. The above evidence does not provide evidence that undue experimentation would be required to produce a bicistronic construct that can produce both HEXA and HEXB.

4. HEX species

The Examiner cites Hammer et al. (1990, Cell 63:1099-1112) to argue the unpredictability of using HEX- α and HEX- β from any species of animal. Hammer et al. (1990) demonstrated that transgenic expression of human HLA-B27 and human β 2-microglobulin (h β 2m) did not result in spondyloarthropathies in mice, whereas it did in humans. However, while the mice did express the transgenes, the mice were not susceptible to the pathologies of B27-associated disease. This is not evidence of unpredictable species compatibility for a given protein. Rather, this is an example of an incompatible host organism as an appropriate model of a human disease. Further, while one cannot *always* predict that a protein from one species will have a similar effect in another species of animal, the composition claims do not recite use in humans *per se*. Thus, if a mouse HEX gene does not treat Tay-Sachs in humans, it still has utility for research in mice.

D. Delivery of HEX constructs

The Examiner argues that the selection of other transposition systems, inducible systems, other promoters, or vectors, would require undue experimentation in order to effectively deliver HEXB-HEXA constructs to cells. As stated above, the enablement standard, when properly applied to the composition claims, requires that one be able to make and use the HEXB-HEXA constructs without undue experimentation. Applicants have addressed each of the Examiner's issues related to this line of argument in kind, but maintain that it is inappropriate to read these types of limitations or issues onto the present composition claims. Applicants have provided one way of making and using the claimed constructs and this way has been shown to be effective. There is absolutely no legal basis for also trying to require the Applicants to teach all ways to make and use their constructs, as the Examiner is currently doing. It is irrelevant whether the "claims read on transposition" this is a mechanism of integration of the claimed compositions and as the Applicants have not claimed this method it is completely irrelevant to whether the present claims are enabled. In fact, even if it was known that the compositions could not be used

in a transposable element (which Applicants are not saying) it still would not invalidate the claims as they stand because the Applicants have taught a mechanism for making and using the claimed compositions. This is all that is required. Nothing more. Applicants have also not explicitly described using the compositions on Mars, which someone currently might fail at, but this no more invalidates the present claims than the fact that someone might try to use the compositions in a transposable element, and they might fail, but this does not mean the claims lack enablement because applicants have provided a method of making and using the claimed compositions which will work for the entire breadth of the claim.

1. Inducer

As stated above, substantive argument on this issue is not needed, but corrections to erroneous statements made by the Examiner are provided. The Examiner cites Wang et al. (1995, PNAS USA 91:8180-8184) and Heikinheim and Kekkonen (1993, Ann Med, 25:71-76) to argue the requirement for undue experimentation to use inducible systems such as RU486 *in vivo* to affect the nervous system.

The Examiner cites Wang (1995) and Heikinheim and Kekkonen (1993) as evidence that RU486 has not been applied to the nervous system and does not cross the blood-brain barrier. However, these references actually say that RU486 *does* cross the blood-brain-barrier, it is just restricted. For example, the concentration of RU486 in the brain was 28% of serum levels (Heikinheim and Kekkonen, 1993).

E. Promoters

The Examiner cites Cowan et al. (2003, Xenotransplantation 10:223-231) to argue the unpredictability in selecting cell-specific promoters from any species without undue experimentation. Thus, the Examiner states that the claimed invention is limited to only rat NSE promoter and rat COL1A1 promoter. However, Cowan et al. (2003) only demonstrates “exception[s] to the general rule” (i.e., ICAM-2, PECAM-1, and endoglin) for the reproducible

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specificity and activity of promoters in transgenic mice and pigs. Cowen actually supports the proposition regarding promoters put forth by the Applicants as a “general rule.” Furthermore, as discussed above, selection of a suitable promoter would not be considered undue experimentation to the skilled artisan, anymore than the skilled artisan would find the selection of a specific monoclonal antibody undue (which was found not to be undue experimentation nearly 20 years ago). One of skill in the art would be able to select a suitable cell-specific promoter using routine techniques well known for many years. Further, as the composition claim is not restricted by the species of the target host, one of skill in the art would understand how to select an inducible promoter compatible with the target species. As stated above, just because selection is required, does not mean that the experimentation is “undue”.

The Examiner further cites Goswami (2003, Journal of Molecular Evolution, 57:44-51) to argue that the specification does not teach how to obtain any rat NSE promoter or rat COL1A1 promoter of any size. The Examiner suggests that one cannot make deletion, substitutions or additions to the provided promoter sequences and “necessarily” retain the same activity. The Examiner argues that since the determination of the suitability of a promoter sequence would need to be determined empirically, obtaining a promoter would require undue experimentation. However, the requirement for empirical analysis does not equate with undue experimentation. Further, the Examiner is arguing that one skilled in the art should be expected to select the same promoter sequence as another without guidance. It is unclear on what the Examiner is basing this standard, but this is certainly not the standard set forth in Wands, where the Applicant nor anyone else could identify a single member falling within the genus of antibodies claimed without performing testing.

The specification provides extensive discussion about promoters, both constitutive and regulated. (See for example, p. 53, l. 1 to p. 56, l. 6 where not only constitutive and regulated promoters are discussed generally but multiple specific examples and sequences of different types of each are provided, in for example, SEQ ID NOS: 21-41). The specification provides

more than enough information about promoters for the skilled artisan to use any type of promoter that may be desired.

Furthermore, the skill in the art, with respect to promoters is extensive. Certainly since the isolation of the CMV promoter and its use in expression of a heterologous construct system, back at least as of January. 30, 1985, (United States Patent No. 5,385,839 for "Transfer vectors and microorganisms containing human cytomegalovirus immediate-early promoter regulatory DNA sequence" and 5,168,062 for "Transfer vectors and microorganisms containing human cytomegalovirus immediate-early promoter-regulatory DNA sequence") the skill of the identification and use of both constitutive and regulatable promoters has only grown. The use of constitutive and cell-specific promoters is well established in the art and the selection of these promoters requires only routine experimentation to evaluate the expression and effects of the selected promoter and transgene.

1. Viral and Non-viral Vectors

The Examiner cites Wolff et al. (1990, *Science*, 247:1465-1468) and Nicolau et al. (1983, *PNAS USA*, 80:1068-1072) and Abdallah et al. (1995, *Biol Cell.*, 85:1-7) and Somia and Verma (2000, *Nature Reviews*, 1:91-99) to argue the unpredictability of non-viral delivery of DNA to specific tissues, such as the brain, in an animal.

The Examiner uses the fact that intravenous delivery of non-viral DNA vectors suspended in liposomes results in localization to the liver and spleen (Nicolau et al., 1983) to argue that non-viral DNA vector may require direct injection into the brain, and at multiple sites, to affect Hex deficiency. However, Abdallah et al. (1995) described the capacity of the brain to take up and express naked DNA (page 5, 2nd column, lines 1-5; Table 1) or DNA in cationic polymers (page 4, 2nd column, lines 13-16; Table 1). Further, while it may be true that the use of non-viral vectors results in inefficient and transient gene-transfer (Somia and Verma, 2000), all that is required for the present claims is that a non-viral vector *can* be used to deliver HEXA and HEXB to a cell.

The Examiner cites Somia and Verma (2000, *Nature Reviews*, 1:91-99) to argue the unpredictability of viral vectors. This review outlines the advantages and disadvantages associated with retroviral vectors, lentiviral vectors, adeno-associated viral vectors, and adenoviral vectors. For example, viral vectors elicit cellular and humoral immunity to transduced cells and vectors, respectively. This is especially true for adenoviral vectors as retroviral, lentiviral and AAV vectors are less immunogenic. However, this review indicates that alternative viral serotypes can be used to overcome host immunity when multiple administrations are required. Finally, the Examiner has not provided any evidence that any viral vector *could not* deliver HEXA and HEXB to cells, even cells in the brain.

VI. Rejection under 35 U.S.C. § 112, first paragraph - Written Description

Claims 1-43, 72-75, 83-91, and 133-141 are rejected under 35 U.S.C. § 112, first paragraph, for allegedly failing to comply with the written description requirement. The Examiner argues that the claim(s) contain subject matter not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The Examiner states that the specification provides adequate written description for the isolated nucleic acid sequences designated as SEQ ID NOs:1, 3, 5, 69, 70, and 71. However, the Examiner argues that the specification fails to describe the relevant identifying characteristics of all the nucleic acid sequences which hybridize and function as HEX-β or teach what part of 70% of SEQ ID NO:3 would need to remain intact in order for the protein to function. The following is a review of the written description standard and a discussion of sequence homology.

Applicants note that it appears that while the Examiner indicates he has reviewed Applicants arguments, the statements and present rejections would indicate otherwise, or at least that Applicant failed in explaining their position, as Applicants previous arguments directly address the present rejection. In this regard, Applicants have restated these arguments below and respectfully request that the Examiner focus on the evidence that has been submitted by the Applicants showing scientifically, that the Examiner's concerns regarding the "functioning" of a

variant protein are unfounded. In addition, Applicants have also tried to address the new arguments provided by the Examiner regarding hybridization and conservative substitutions.

A. Written Description Law

While there are many aspects and nuances to the courts' interpretation of the written description requirement under 35 U.S.C. § 112, first paragraph, only those aspects directly addressing the legal position of the Office Action are addressed. The Office Action correctly states that one can adequately meet the requirements of the written description requirement by "describing the invention with sufficient relevant identifying characteristics (as it relates to the invention as a whole) such that a person skilled in the art would recognize that the inventor had possession of the claimed invention" (citing Pfaff v. Wells Electronics, Inc. 48 USPQ2d 1641, 1646 (1998), *emphasis in original*). However, contrary to the position of the Office Action, this standard does *not* require that "conception is not achieved until reduction to practice has occurred" (Office Action, p. 23). No case that the Examiner has relied upon supports this position, and furthermore, there is none that the Applicant is aware.

It has been repeated over and over by the Federal Circuit that "the written description requirement can be met by "show[ing] that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics ... i.e., complete or partial structure, other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics." Enzo Biochem vs. Gen-Probe Incorporated, 296 F.3d 1316, 1324, 63 U.S.P.Q.2d 1609 citing the Written Description Guidelines, 66 Fed. Reg. at 1106. As noted by the Examiner, this standard, as well as many others is viewed through the eyes of the skilled artisan. As discussed below, there can be no doubt that claims 1-43, 72-75, 83-91, and 133-141 meet this standard.

Regents of the University of California v. Eli Lilly and Company, 119 F.3d 1559, 1567, 43 U.S.P.Q.2d 1398 (Fed. Cir. 1997) held that a method of obtaining an unknown gene was not adequate written description for the gene itself when nothing was known about the structure of the gene itself. As will be discussed below, this is factually very different than the compositions

of claims 1-43, 72-75, 83-91, and 133-141, where structure is known and provided in the specification.

A patent application preferably omits that which is well-known or common knowledge to those of ordinary skill in the art.¹ Thus, an applicant should not be penalized for leaving out information in his patent application that those of ordinary skill in the art knew or could readily have obtained at the time of the filing of the patent application.

B. Homology

The USPTO has already established that variants can be claimed based on sequence identity (see Example 14 of the U.S.P.T.O. “Synopsis of Application of Written Description Guidelines”), wherein it is stated:

“[t]he single species disclosed is representative of the genus because all members have at least 95% structural identity with the reference compound and because of the presence of an assay which applicant provided for identifying all of the at least 95% identical variants...which are capable of the specified catalytic activity.”
(page 54, fourth paragraph)

For the sake of argument, in a complex sequence, the issue of *envisioning all members* with 95% identity, which the Examiner is concerned with, would also be present, as it is allegedly present for compositions having 70% identity. The PTO has understood, however, in the issuance of the Guidelines, that “envisioning” all members is not the standard for written description nor is it required. (Applicants note that if required, however, every sequence having 70% identity to SEQ ID NO:1 or 3 could be written out, merely by the recitation of SEQ ID NO:1 and 3. Although there would be many, many sequences and it might take someone many years to actually sit and write each on a piece of paper, a high school biology student with the genetic code table in one hand and a systematic method of making each substitution in the other,

¹ “[A] . . . specification need not disclose what is well known in the art.” (*Lindemann Maschinenfabrik v. Am. Hoist and Derrick*, 730 F.2d 1452, 1463 (Fed. Cir. 1984) (citing *In re Myers*, 410 F.2d 420 (CCPA 1969). See also *Hybritech Inc. v. Monoclonal Antibodies, Inc.* 802 F.2d 1367, 1384 (Fed. Cir. 1986).

could write each sequence. This point will not be argued further, however, as the standard does not require this).

The issue then becomes, if the principle of defining a genus of genetically related compositions by their identity is a viable way of describing a genus because the genus all has a common structural identity, then the only thing left is the extent of the functional identity that should be allowed in claims 12 and 16.

In this regard, it is generally understood that a molecule with 70% or greater homology to a known sequence will have the essential physical properties of the identified structure. For example, it has been demonstrated using pairwise sequence comparison that enzyme function is well conserved when a sequence identity is above 40%, and more importantly that 60% identity is sufficient for at least 90% retention of functional conservation, and that enzyme function does not *start* to diverge, *at all*, until the sequence identity is below 70% (see Tian, W. and Skolnick, J. J Mol Biol. 2003 Oct 31;333(4):863-82, attached herewith). Thus, contrary to the Examiner's position that the Applicant won't know which sequences function and which do not, at 70% identity, the Applicant would expect with a very high level of certainty that any given sequence would function, and this is assuming that no information about amino acids that are important for function is known (which is not the facts in the present application, as discussed extensively through out the present application certain mutations are well known to cause neurodegenerative diseases). If one factors in this knowledge to the analysis, the skilled artisan would likely never pick a sequence that would not function.

Further, while the skilled artisan has a high expectation that any given sequence having 70% identity would function, if needed, it is routine experimentation for one skilled in the art to test such variants to determine if they fit into the claimed homology and to assay said variant for functionality. Provided there is some type of assay in the specification, such as a model system to assay the disclosed compositions. The specification states:

"A model system for the study of these vectors is a mouse that is knockout mouse deficient in both HexA and HexB, since the *hexA*^{-/-}/*hexB*^{-/-} mouse is characterized by global disruption of the *hexA* and *hexB* genes. Gene disruption in this mouse is

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global, and therefore, can be used as a model for global replacement.” (Page 41, lines 18-21).

Thus, the concerns of the Examiner, that not all members can be envisioned and that there is no way to determine which members have functional activity, can be removed.

Contrary to position of the Office Action with respect to Fiers v. Revel, 25 USPQ2d 1601, 1606 (Fed. Cir. 1993), Amgen Inc. v Chugai Pharmaceuticals Co. Ltd., 18 USPQ2d 1016 (Fed. Cir. 1991) and Fiddes v. Baird, 30 USPQ2d 1481, 1483, reduction to practice of each member of a genus is not required. Furthermore, Fiers, Amgen, and Fiddes, all support the state of the law as set forth in Lilly and Enzo, for example, that some structure with a means to identify the function of members of the genus is sufficient to describe a genus of compounds that are both structurally and functionally related, such as the structures set forth in claims 1-43, 72-75, 83-91, and 133-141. Furthermore, as discussed above, in the present application, these cases can also be distinguished in that the structure of the composition being claimed is provided in the specification, and in Fiers and Lilly, the structure of the composition being claimed was unknown. Applicants also respectfully point out that the reference to “conception” in the context of the present rejection is misplaced as the rejection is not dealing with a 35 U.S.C. 102(g) rejection as was the case in certain subparts of both Fiers and Amgen.

Thus, for claims which are limited by a percent identity as discussed herein, there can be no written description issue as set forth by the Examiner because the “functional” issues worrying the Examiner do not exist for proteins having at least 70% homology because they almost all will function irrespective of where the variation occurs. Furthermore, the for claims not so limited, as discussed above there is absolutely no requirement that the applicant be able to envision all species. The Applicant must enable all species, which the Applicant has here done. As discussed above, it is not undue experimentation to test variants for activity. If it were, Wands would have been held differently, because Wands did not know a single structure of any of his antibodies, even after he had isolated them, much less before he did. This simply cannot be the law.

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The Applicant respectfully requests the withdrawal of the rejection, and allowance of claims 1-43, 72-75, 83-91, and 133-141.

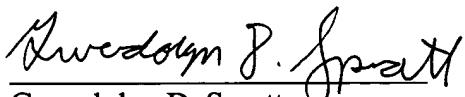
VII. Rejection under 35 U.S.C. § 112, second paragraph

Claim 11 is rejected under 35 U.S.C. § 112, second paragraph, as allegedly lacking sufficient antecedent basis for the limitation “the second IRES sequence is located 3’ to the other parts” in the claim. The second paragraph 35 U.S.C. § 112 requires that the claims particularly point out and distinctly claim the subject matter which the applicant regards as his invention. It is the Applicant’s position that one of skill in the art reading this claim would understand “other parts” to be referring to the nucleic acid encoding HEX- α and HEX- β , the IRES, and the promoter of the preceding claims to which it depends. For example, claim 8 recites “wherein the parts are oriented 5’-promoter-HEX- β encoding sequence-IRES- HEX- α encoding sequence-3’.” All that is required is that the claim be clear as to what is claimed, which the Applicant contends is the case in the instant claim.

A Request for a Two Month Extension of Time and a Credit Card Payment Form PTO-2038 authorizing payment in the amount of \$225.00, for the two month extension of time, are enclosed. This amount is believed to be correct; however, the Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 14-0629.

Respectfully submitted,

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How Well is Enzyme Function Conserved as a Function of Pairwise Sequence Identity?

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Enzyme function conservation has been used to derive the threshold of sequence identity necessary to transfer function from a protein of known function to an unknown protein. Using pairwise sequence comparison, several studies suggested that when the sequence identity is above 40%, enzyme function is well conserved. In contrast, Rost argued that because of database bias, the results from such simple pairwise comparisons might be misleading. Thus, by grouping enzyme sequences into families based on sequence similarity and selecting representative sequences for comparison, he showed that enzyme function starts to diverge quickly when the sequence identity is below 70%. Here, we employ a strategy similar to Rost's to reduce the database bias; however, we classify enzyme families based not only on sequence similarity, but also on functional similarity, i.e. sequences in each family must have the same four digits or the same first three digits of the enzyme commission (EC) number. Furthermore, instead of selecting representative sequences for comparison, we calculate the function conservation of each enzyme family and then average the degree of enzyme function conservation across all enzyme families. Our analysis suggests that for functional transferability, 40% sequence identity can still be used as a confident threshold to transfer the first three digits of an EC number; however, to transfer all four digits of an EC number, above 60% sequence identity is needed to have at least 90% accuracy. Moreover, when PSI-BLAST is used, the magnitude of the *E*-value is found to be weakly correlated with the extent of enzyme function conservation in the third iteration of PSI-BLAST. As a result, functional annotation based on the *E*-values from PSI-BLAST should be used with caution. We also show that by employing an enzyme family-specific sequence identity threshold above which 100% functional conservation is required, functional inference of unknown sequences can be accurately accomplished. However, this comes at a cost: those true positive sequences below this threshold cannot be uniquely identified.

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Keywords: genome annotation; conservation of protein function; enzyme classification; sequence comparisons; PSI-BLAST

Introduction

In this post-genomic era with many sequenced genomes, functional annotation has become a major aim of Bioinformatics.^{1–7} The most widely used functional annotation scheme is based on two steps. The first step is to detect a homologous relationship between pairs of proteins; this can be accomplished by a pairwise sequence similarity

search with algorithms such as FASTA,⁸ BLAST⁹ and PSI-BLAST.¹⁰ The second step of functional annotation is to infer functional similarity from homology. With the continuing development of those methods, the ability of recognizing remote homologies has been greatly improved. However, because there might be only about 1000 major superfamilies in nature,^{11,12} most homologous (viz. evolutionarily related) proteins must have different functions, which makes the inference of functional similarity from sequence similarity difficult and perhaps problematic.^{13,14} With the rapidly increasing number of completely sequenced genomes

Abbreviation used: EC, enzyme commission.

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and the efforts to annotate gene function, annotation errors could be easily spread if functional annotation is not done carefully; thus, systematic studies that establish the accuracy and reliability of methods that infer functional similarity from homology are urgent and necessary.

Percentage sequence identity and statistical score, such as *E*-value of BLAST or FASTA, are widely used measures for sequence comparison. It has been well established that scores based on the statistical significance relative to random are superior to percentage sequence identity in detecting remote homology.¹⁵ However, there is no clear indication of whether this is also true with respect to assessing functional relationship. In fact, it has been frequently observed that function starts to diverge quickly even at high level of sequence identity at which there is no dispute about homology.^{16–20} On the other hand, as a quick and simple measure, sequence identity is also widely used as an indication of functional similarity. For example, it is often implicitly used in dividing a protein family into subfamilies by constructing a phylogenetic tree to derive functionally important residues.^{21–24} However, because the lack of a rigorously established sequence identity threshold, the division of a protein family into subfamilies may require human intervention.^{24,25} Therefore, it is of great significance to establish the threshold of sequence identity above which functional similarity can be affirmed.

Because the Enzyme Commission (EC) is the best developed and most widely used functional classification scheme,²⁶ EC numbers have been employed to explore the threshold of sequence identity necessary for accurate function transfer. EC numbers classify the function of an enzyme by four digits. The first digit delineates the main type of enzymatic activity and ranges from 1 to 6: 1, oxidoreductases; 2, transferases; 3, hydrolases; 4, lyases; 5, isomerases; and 6, ligases. The other three digits provide more detail about the reaction that an enzyme catalyzes. The last digit of an EC number usually represents the substrate specificity of a reaction, while the first three digits of the EC number usually describe the overall type of enzymatic reaction. By conducting all-against-all pairwise sequence comparisons and examining EC number match at different sequence identity thresholds, Devos,²⁰ Wilson,¹⁸ and Todd¹⁷ observed that enzyme function is well conserved. Devos took structure alignments from the FSSP (families of structurally similar proteins) database²⁷ and discovered that above 50% sequence identity, all four digits of an EC number are well conserved. Wilson performed pairwise sequence, structure and function comparisons on protein domain pairs according to the SCOP (Structural Classification of Proteins) fold classification²⁸ and found that full conservation of all four EC digits can occur between two proteins with as low as ~40% sequence identity. Todd assessed the functional variation of homologous enzyme superfamilies defined by the CATH (protein class, architecture,

topology and homologous superfamily classification) protein structure classification²⁹ and found that functional variation is rare when the sequence identity is above 40%. Thus, it seemed that 40% sequence identity might be used as a confident threshold for assessing functional conservation.

In contrast, a recent study by Rost¹⁹ argued that the SWISSPROT database,³⁰ which has been used as a gold standard for the functional annotation of the other databases,^{31–34} has many redundant sequences that cover just a small fraction of enzyme functions. Thus, SWISSPROT is a biased database dominated by a few functional families, and the results of enzyme function conservation based only on simple pairwise comparison might be misleading. To reduce the bias in the SWISSPROT database, Rost classified enzyme sequences into families on the basis of their sequence similarity, or detectable evolutionary relationship. Usually, two proteins that are structurally similar to each other are considered as evolutionarily related. It has been established that when the pairwise sequence identity between two proteins is above 30%, they have similar structures and are evolutionarily related.^{35–37} However, the relationship between sequence–structure similarities is not clear when the pairwise sequence identity is below 30%, especially in the “twilight zone” (<25% sequence identity).^{35–37} To extend sequence comparison into the twilight zone, Rost employed the HSSP (homology-derived structures of proteins) score (a score derived from sequence identity to indicate whether two sequences might have similar structures) to measure the sequence similarity between two proteins.^{36,38} He grouped enzyme sequences retrieved from the SWISSPROT database into sequence families based on their HSSP score and then selected representative sequences to construct an unbiased dataset. Finally, enzyme sequences from the unbiased dataset were compared with those from the original dataset to calculate the extent of enzyme function conservation. Rost showed that when the sequence identity is below 70%, both the first digit and all four digits of EC numbers start to quickly diverge,¹⁹ a significantly different conclusion from that of previous studies. This discrepancy in the threshold of enzyme function conservation has raised questions about whether current functional annotation schemes based on sequence similarities can be trusted. Thus, additional evaluation of enzyme function conservation is timely and important.

Obviously, by classifying enzyme sequences into families to reduce the bias, the conclusions of Rost should be closer to the truth. Presumably, a family of sequences should have a clear evolutionary relationship and be functionally similar to each other. However, because the relationship between functional divergence and sequence divergence is in fact not clear (a point that is further addressed here), using only sequence similarity to classify protein families might result in one family being linked to different kinds of function. In fact, it has

been frequently observed that function may diverge more quickly than sequence, and homologous proteins may evolve to have different functions and possess different functional sites, especially when sequence identity falls below 40%.^{17,18,20,39} Thus, the dataset constructed by Rost that contains only representative sequences might miss some enzyme functions in the calculation of functional conservation. Furthermore, the presence of various functions in one family may also make it difficult to accurately transfer function to new sequences.

Here, we employ both functional similarity and sequence similarity to define a protein family. Instead of trying to define functional similarities, we directly use the functional annotation in the SWISSPROT database and define an enzyme family as a family of sequences that are all above a certain threshold of pairwise sequence similarity and that also have the same function. Enzyme function is defined at two levels: by conservation of the full four digits of the EC number, which include the substrate specificity and more detailed information, such as cofactor or metal of a particular enzyme reaction, and by conservation of the first three digits of the EC number, which generally has a less detailed description of a particular type of enzyme reaction. Employing these criteria, we have classified all enzyme sequences (excluding those sequences with multiple EC numbers, or undetermined EC digits, or identified only by sequence similarity using computational methods) in the SWISSPROT database. We calculate the functional conservation rate of each family by collecting all possible sequence pairs related to the family in the SWISSPROT database at different thresholds of sequence identity and then compare their functional annotation. Finally, we average the enzyme function conservation across all the enzyme families. Our results suggest that for functional annotation, 40% sequence identity can still be used as a confident threshold to transfer the first three digits of an EC number. However, to transfer all four digits of an EC number, above 60% sequence identity is needed to have above 90% accuracy. Moreover, we find that the threshold of the *E*-value for enzyme function conservation changes significantly during the PSI-BLAST iteration process, and in the third iteration of PSI-BLAST, the *E*-value shows only a weak correlation with functional conservation. Furthermore, by conducting a jack-knife analysis, we find that by employing an enzyme family-specific threshold above which 100% functional conservation is required, functional inference of unknown sequence from known sequence can be done accurately. However, because 100% conservation rate is required for establishing the threshold, true positive sequences that have a sequence identity to sequences of known function lower than the threshold cannot be identified. Finally, we apply the family-specific threshold to KEGG annotated enzyme sequences and find that about 58% and

65% of KEGG enzyme sequences can be confirmed with 100% confidence at full four EC digits and the first three EC digits level, respectively. All of our results can be downloaded from our website†.

Results

The conservation of all four digits of the EC numbers is lower than previously anticipated, while the first three digits of the EC numbers are still well conserved

We have calculated the average degree of enzyme function conservation across all the classified enzyme families over different ranges of pairwise sequence identity. To investigate the effects of the definition of sequence identity on the extent of enzyme function conservation, we conduct the calculation based on the global identity, the big identity, the small identity, and the aligned identity of the MM alignment, and the sequence identity reported by the PSI-BLAST alignment, respectively (the definitions of the various types of sequence identity can be found in Methods: Measurements of sequence similarity). The results are shown in Figure 1. It can be clearly seen that: (1) the global identity has the strongest correlation to the degree of enzyme function conservation, while the correlation of the aligned sequence identity of the MM alignment and PSI-BLAST sequence identity to enzyme functional conservation is worse than the other three definitions of sequence identity. For example, for enzyme–enzyme only comparisons, when the pairwise sequence identity falls into the 50–60% range, the conservation rate of the full four digits of an EC number is 87% when the global identity is used, while it is only 68% and 78% when the aligned identity of the MM alignment and the PSI-BLAST identity are used, respectively (Figure 1A). Moreover, when the pairwise sequence identity is in the 40–50% range, the conservation rate of the first three digits of an EC number can still be 93% when the global identity is used, while it is only 74% and 72% when the aligned identity of the MM alignment and the PSI-BLAST identity are used, respectively (Figure 1C). Because the global identity has the strongest correlation to enzyme functional conservation, it is used in what follows to study how well the enzyme function is conserved.

(2) The conservation of the full four digit EC number is lower than previously anticipated, while the first three digits of the EC numbers are still well conserved. Following the strategy used by Devos,²⁰ Wilson,¹⁸ and Todd,¹⁷ we also conduct a simple all-against-all pairwise sequence comparison without family classification and employ the global identity to calculate the enzyme function

† http://bioinformatics.buffalo.edu/resources/enzyme_conservation

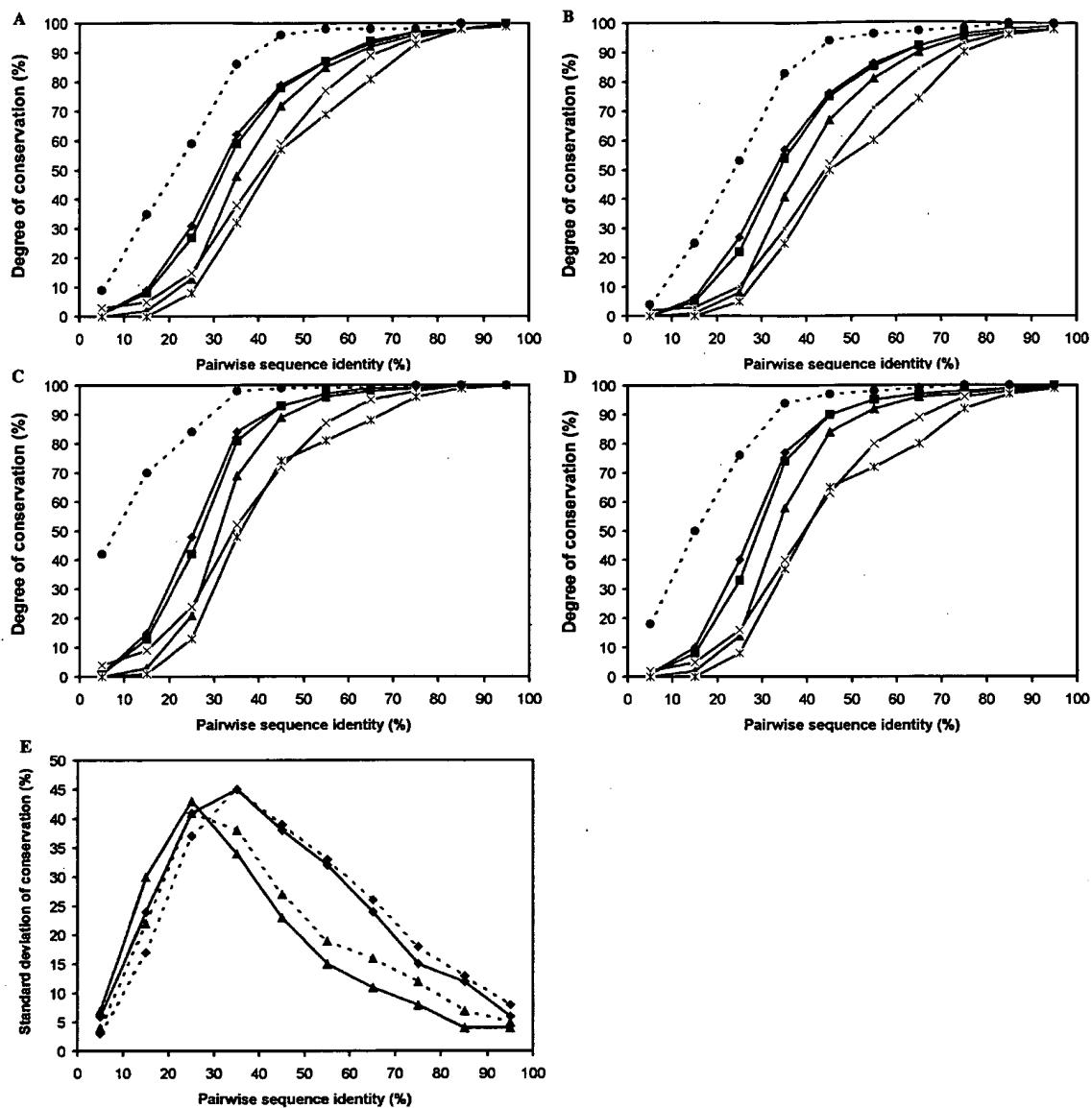


Figure 1. The enzyme function conservation in terms of sequence identity. Two pools of sequence pairs are used to derive the extent of enzyme function conservation: one that includes only enzyme–enzyme sequence pairs (A and C), and another that includes both enzyme–enzyme and enzyme–non-enzyme sequence pairs (B and D). The extent of functional conservation is calculated at two levels of enzyme functions: the all four EC digits (A and B), and the first three EC digits (C and D). In calculating the extent of enzyme function conservation, the functional conservation of each enzyme family is calculated first and then is averaged across all enzyme families. To investigate the effects of the definition of sequence identity on enzyme function conservation, five definitions of sequence identity are used: the global sequence identity (diamond symbol in continuous line, \blacklozenge), the big sequence identity (square symbol in continuous line, \blacksquare), the small sequence identity (triangle symbol in continuous line, \blacktriangle), and the aligned sequence identity of the MM alignment (star symbol in continuous line, \star), and the reported sequence identity of the PSI-BLAST alignment (cross symbol in continuous line, \times). (The definitions can be found in Methods: Measurements of sequence similarity.) To compare with the previous estimation of enzyme function conservation, a simple all-against-all pairwise sequence comparison without family classification is conducted using the global sequence identity (circle symbol in broken line, \bullet). The standard deviation of enzyme function conservation as a function of global sequence identity is shown in E. The standard deviation of the conservation of all four EC digits and the first three EC digits are shown with diamond symbol (\blacklozenge) and triangle symbol in continuous line (\blacktriangle), respectively, with the continuous line and broken line representing the results in the condition of only enzyme–enzyme comparisons and both enzyme–enzyme and enzyme–non-enzyme comparisons, respectively.

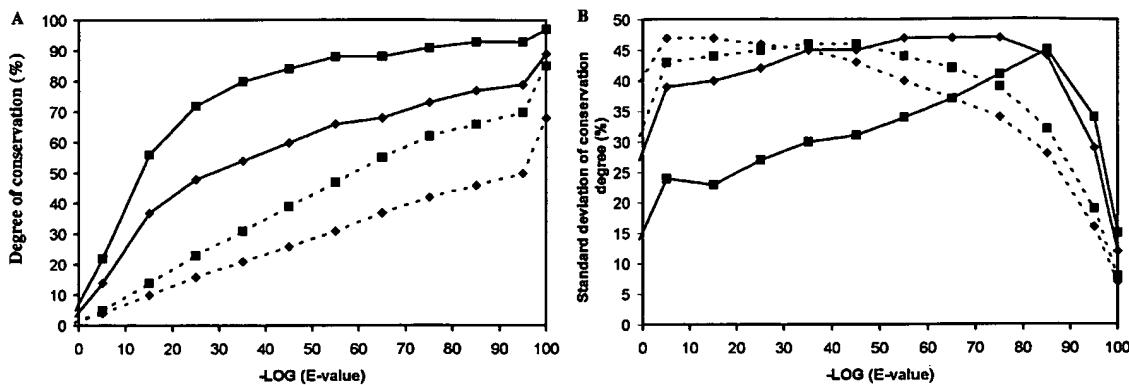


Figure 2. The enzyme function conservation in terms of the PSI-BLAST *E*-value. Following a similar strategy to calculate the enzyme function conservation in terms of sequence identity, the PSI-BLAST *E*-value is used to evaluate the extent of enzyme function conservation. A, The result of function conservation in terms of PSI-BLAST *E*-value when only enzyme–enzyme comparisons are used, with the standard deviation shown in B. Two sets of PSI-BLAST *E*-value are employed. The square symbol (■) and the diamond symbol (◆) in continuous line represent the results of the full four EC digits conservation and the first three EC digits conservation, respectively, when the PSI-BLAST *E*-value obtained in the first round of PSI-BLAST search is used. The triangle symbol (▲) and the cross symbol (×) in the broken line represent the results of the full four EC digits conservation and the first three EC digits conservation, respectively, when the PSI-BLAST *E*-value obtained in the third round of PSI-BLAST search is used.

conservation. Similar to the previous observations, for all-against-all enzyme–enzyme comparison, the conservation rate of the full four digits of an EC number can still be 96% when the global identity is in the 40–50% range, while the conservation rate of the first three digits of an EC number is 98% when the global identity falls in the 30–40% range (Figure 1A and C). In contrast, following our strategy to reduce the bias in the SWISSPROT database by both sequence and functional similarity, we find that for enzyme–enzyme comparisons, the conservation rate of the full four digits of an EC number starts to be below 90% when the global identity is below 60% (Figure 1A); this makes the extent of conservation of all four digits of an EC number lower than previously anticipated. However, the first three digits of an EC number are still well conserved; for enzyme–enzyme only comparisons, the average conservation rate of the first three digits of an EC number can still be 93% in the range of 40–50% of global identity (Figure 1C). This result is in contrast to Rost's observation that both the full four digits and the first digit of an EC number start to diverge when sequence identity is below 70%.¹⁹ When enzyme–non-enzyme comparisons are also included in the calculation, we find that the degree of function conservation is a little lower than that when only enzyme–enzyme comparison is counted (Figure 1B and D). However, the degree of function conservation for the full four digits and the first three digits can still be above 90% when the global identity is above 60% and 40%, respectively (Figure 1B and D).

Thus, our analysis suggests that for function transferability, 40% global identity can still be used as a confident threshold to transfer the first

three digits of an EC number; however, to transfer the full four digits of an EC numbers with above 90% accuracy, then above 60% global identity is required.

The *E*-value at the third iteration of PSI-BLAST has a weak correlation to enzyme function conservation

Following the similar strategy used to calculate the enzyme function conservation as a function of the global identity, we also calculate the enzyme function conservation as a function of the PSI-BLAST *E*-value, e.g. e^{-60} – e^{-50} (Figure 2). Our results show that the *E*-value in the third iteration of the PSI-BLAST search has a weak correlation to the degree of enzyme function conservation. For example, for enzyme–enzyme comparison, even when the *E*-value is less than e^{-100} , the average conservation rate of the full four digits and the first three digits of an EC number is only 68% and 85%, respectively (Figure 2A).

In contrast, the *E*-value in the first round of the PSI-BLAST search has a much better correlation to enzyme function conservation. For example, the average function conservation rates of all four digits and the first three digits of an EC number are 89% and 97%, respectively, when the *E*-value is less than e^{-100} in the first round of the PSI-BLAST search. Moreover, the average conservation rate of the first three digits of an EC number can be 88% when the *E*-value is between e^{-60} and e^{-50} in the first round of the PSI-BLAST search, in contrast to only around 47% in the third iteration of the PSI-BLAST search in the same *E*-value level (Figure 2A). The significant changes of the threshold of *E*-value for enzyme function conservation

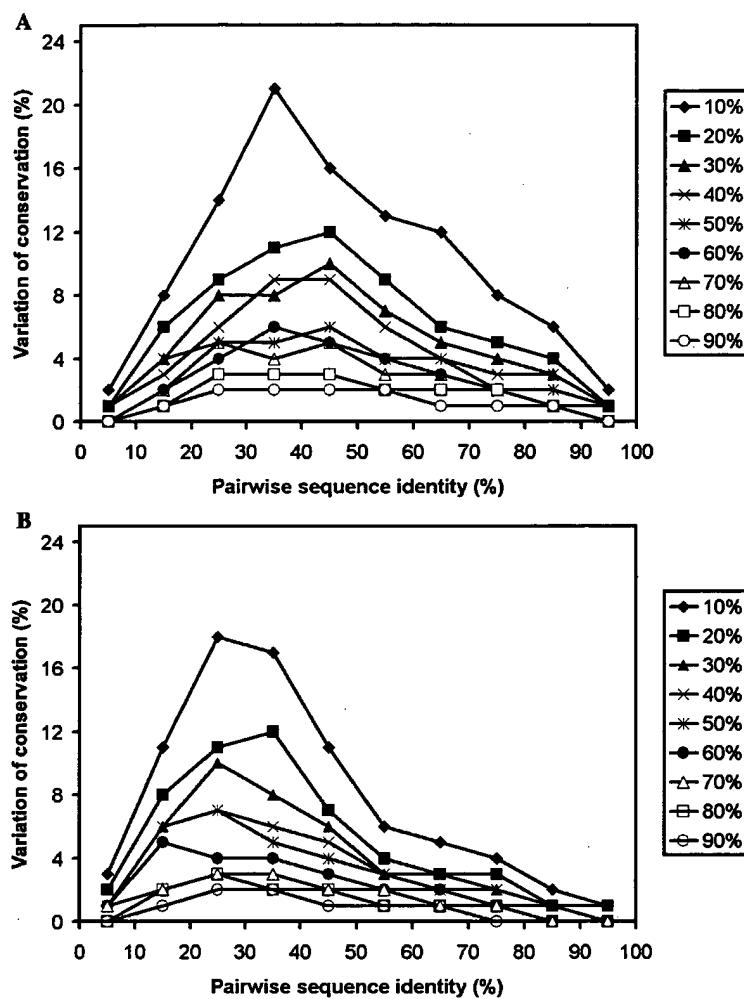


Figure 3. The variation of function conservation by the selection of enzyme families. A, The conservation variation of full four EC digits by using different subsets of full four EC digits enzyme families at different levels of sequence identity. B, The conservation variation of the first three EC digits by using different subsets of the first three EC digits enzyme families at different levels of sequence identity.

at different steps of PSI-BLAST search suggests that *E*-value is not a good measure for transferring functions by PSI-BLAST.

The average enzyme function conservation does not differ by the selection of enzyme families

Figures 1E and 2B show the standard deviation of conservation rate at different levels of sequence identity as a function of the global sequence identity and the PSI-BLAST *E*-value, respectively. Apparently, functional conservation varies among different enzyme families. However, the average enzyme function conservation does not depend on which enzyme families are selected, provided there are a sufficient number of enzyme families considered. When using 10% of the total number of enzyme families, the average conservation rate varies significantly among different subsets (Figure 3A and B). However, when additional enzyme families are included for the calculation, the results

become stable: when using more than 50% of the total number of enzyme families, the variation among different subsets is less than 5% at all level of sequence identity (Figure 3A and B).

When the conservation rate of an individual enzyme family is not 100% at a level of sequence identity, it varies with the selection of enzyme sequences

Although the average enzyme function conservation does not differ with the selection of enzyme families (Figure 3A and B), for an individual enzyme family, generally, the inclusion of more enzyme sequences makes the sequence identity threshold required to accurately transfer function more stable (Figure 4). However, when the sequence identity level is high, there is not much variation of the conservation rate: the average conservation variation for individual enzyme families is less than 5% for all subsets when the global sequence identity is above 60% (Figure 4A).

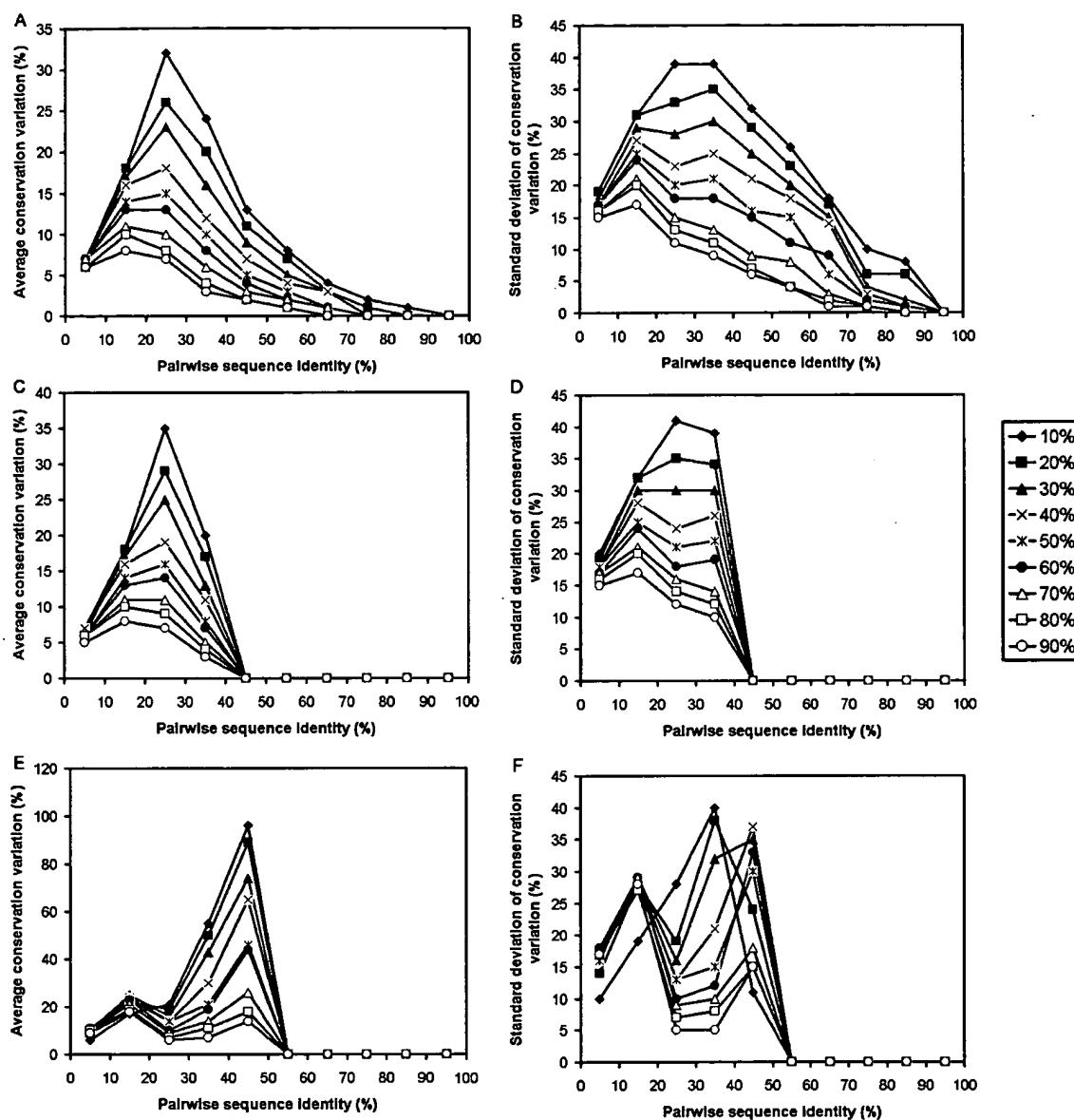


Figure 4. The variation of functional conservation of individual enzyme families by the selection of enzyme sequences. A, C and E show the average conservation variation by using different subsets of enzyme sequences (the symbol for different subsets is shown in the text box) at different levels of sequence identity, for all full four EC digits enzyme families that have more than 30 sequences, those full four EC digits enzyme families that are absolutely conserved above 40% global sequence identity, and those full four EC digits enzyme families that are conserved above 50% but not above 40% global sequence identity, respectively. The corresponding standard deviation of conservation is shown in B, D, and F, respectively.

This is because when the sequence identity is above 60%, the enzyme function tends to be conserved (Figure 1). Actually, when we focus on those enzyme families that are absolutely conserved above 40% global sequence identity, it can be clearly seen that there is no conservation variation for all subsets when the sequence identity is above 40% (Figure 4C). In contrast, when we focus on those enzyme families that are absolutely con-

served above 50% but not above 40% global sequence identity, it can be clearly seen that the function conservation rate varies significantly with the selection of enzyme sequences when the level of global sequence identity is 40–50%: the average conservation variation is around 70% and 20% when 30% and 70% of the total number of known enzyme sequences in the family are used, respectively (Figure 4E). Because there are only a small

number of enzyme families that are absolutely conserved above 50% sequence identity but not above 40% global sequence identity (12 families), it is possible that the conservation variation at 40–50% sequence identity level may change when more enzyme families are used. Nevertheless, the conservation rate of individual enzyme family can vary significantly with the selection of enzyme sequences when it is not 100% conserved at a particular level of sequence identity.

When both enzyme–enzyme and enzyme–non-enzyme are included in the comparison, above 70% and 50% global sequence identity is required to have more than 90% of the enzyme families absolutely conserved at the level of full four EC digits and the first three EC digits, respectively

As we have shown in Figure 4, the conservation rate of an individual enzyme family at a level of sequence identity is sensitive to the selection of enzyme sequences if it is not 100% conserved. Therefore, in order to accurately transfer function from sequence comparison, it is desirable that we use the enzyme family-specific sequence identity threshold above which a 100% conservation rate can be obtained. We have obtained the family-specific sequence identity threshold for all the classified full four EC digits and the first three EC digits enzyme families. As an alternative indication of enzyme function conservation, we plot the percentage of absolutely conserved enzyme families above different sequence identity levels (Figure 5). For enzyme–enzyme only comparisons, when the global identity is above 60% and 40%, there are more than 90% of the enzyme families absolutely conserved at the level of full four EC digits and the first three EC digits EC, respectively. When both enzyme–enzyme and enzyme–non-enzyme comparisons are

included, above 70% and 50% global identity is now required to have more than 90% of the enzyme families absolutely conserved at the level of full four digits and the first three digits of the EC number, respectively. However, there are still more than 70% of the families absolutely conserved at the level of the full four EC digits and the first three EC digits, when the global sequence identity is above 40% and 30%, respectively (Figure 5). This suggests that by using a family-specific sequence identity threshold, the majority of enzyme functions can still be transferred at relatively low levels of sequence identity with confidence. However, we have to point out that the majority of the conserved enzyme families are families with a small number of sequences. Thus, it is possible that the current status of enzyme function conservation might change when more enzyme sequences are deposited into the database.

The enzyme family-specific sequence identity threshold can be used to transfer function accurately from sequence comparison; however, because a 100% conservation rate is required, true positive sequences can be missed

After all, the goal of studying enzyme function conservation is to transfer enzyme functions accurately. To test whether the calculated enzyme family-specific sequence identity threshold can be applied to accurately transfer function, we conduct a jack-knife analysis. The results do not differ by the selection of “training” and “test” sequence for both the full four EC digits and the first three EC digits transfer (Figure 6A and B). Generally, the percentage of “transferable” sequence pairs (the “test”–“training” sequence pair with a sequence identity above the threshold of the family to which the training sequence belongs) decreases with the decrease of the level of sequence identity,

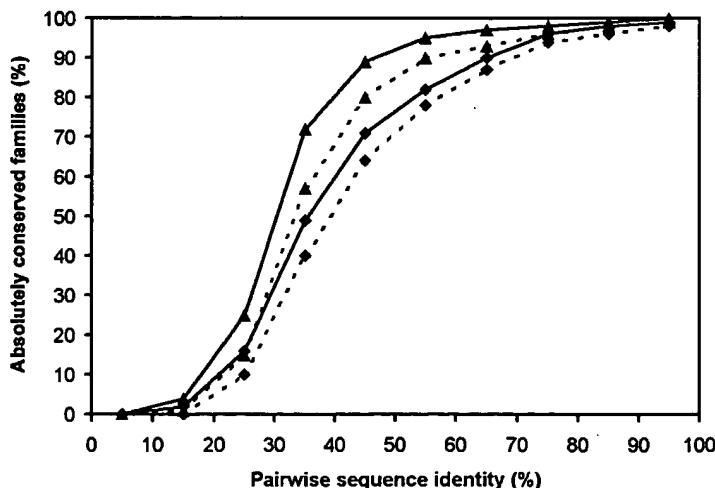


Figure 5. The percentage of 100% conserved enzyme families above different levels of sequence identity. The diamond symbol (◆) and the triangle symbol (▲) represent the results of the full four EC digits and the first three EC digits enzyme families, respectively. The results from only enzyme–enzyme comparisons and from both enzyme–enzyme and enzyme–non-enzyme comparisons are shown as continuous line and broken line, respectively.

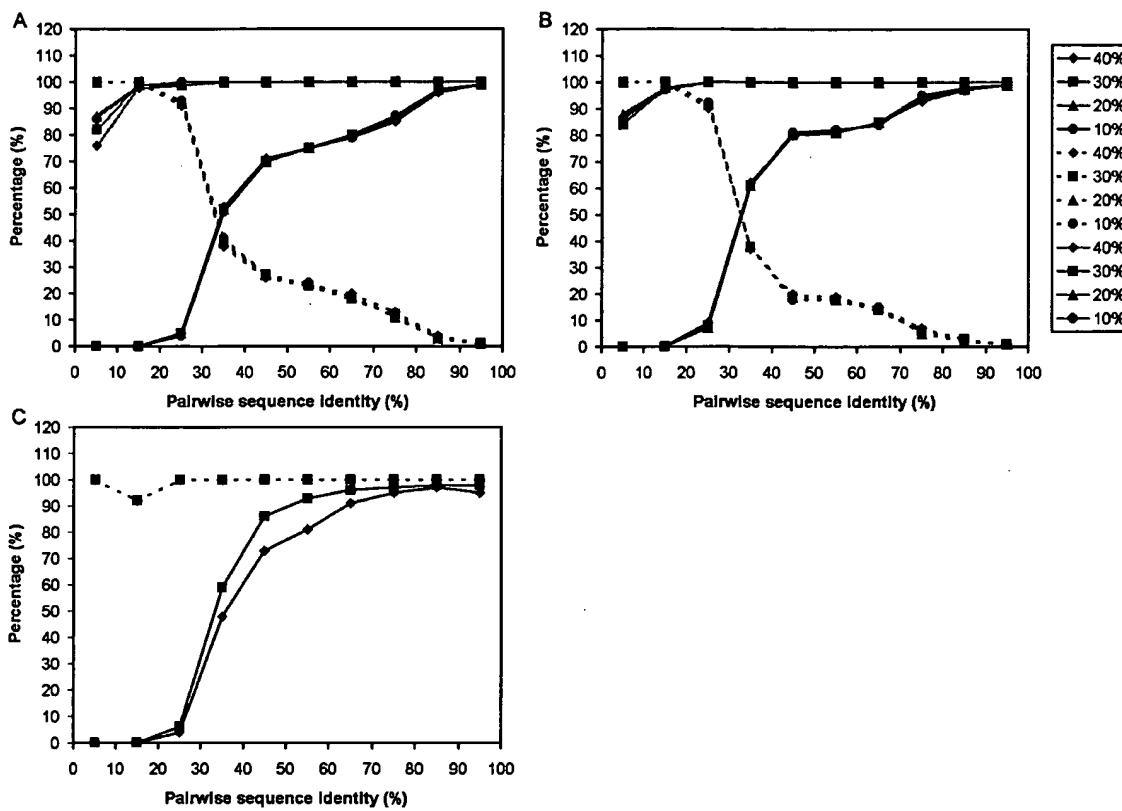


Figure 6. The application of enzyme family-specific sequence identity threshold for functional inference of unknown sequences. The results of jack-knife analysis for the full four EC digits and the first three EC digits transfer are shown in A and B, respectively. The average percentage of transferable sequence pairs, missed sequence pairs, and the prediction accuracy at different levels of sequence identity are shown in continuous line, broken line, and gray line, respectively. The symbols of different test sets are shown in the text box. The standard deviation of the above numbers is small and is not shown here. C, The prediction results of KEGG annotated enzyme sequences by employing the enzyme family-specific sequence identity threshold obtained from the 22,645 SWISSPROT sequences. The diamond symbol (◆) and the square symbol (■) represent the results of the full four EC digits and the first three EC digits prediction, respectively. The percentage of transferable sequence pairs and the prediction accuracy at different sequence identity levels are shown in continuous line and broken line, respectively.

and it drops close to zero when the sequence identity is below 30%. However, it can be clearly seen that despite the decrease of transferable sequence pairs when the global sequence identity drops, the prediction accuracy is not affected by the level of sequence identity: when the sequence identity is above 20%, it is always 100% for both full EC number and the first three EC number transfers (Figure 6A and B). However, the price for accurate functional transfer is that all those true positive test sequences that have a sequence identity with the training sequence below its family-specific identity threshold cannot be identified, and the number increases when the sequence identity drops: at the level of 40–50%, the percentage of the "missed" sequence pairs (the test-training sequence pair with a sequence identity below the threshold of the family of the training sequence but with the same function) is about 30% and 20% for full EC number and the first three EC number transfer, respectively, in contrast to around 40% for both

full EC number and the first three EC number transfer at the level of 30–40% sequence identity (Figure 6A and B). Nevertheless, considering the concerns about the substantial amount of misannotations, it is better to have a small number of "safe" annotations than a large number of "unsure" annotations.

The percentage of transferable sequence pairs at different levels of sequence identity reflects the possibility of transferring functions accurately by employing a family-specific identity threshold given a pair of sequences at a particular sequence identity level. However, we note that the distribution of enzyme sequences in the SWISSPROT database is biased and different from that in a real genome;¹⁹ the test-training sequence pairs here might be dominated by those sequences from a small number of enzyme families. As a result, this probability might change when more enzyme sequences are deposited into the database.

Employing a family-specific sequence identity threshold to evaluate the functional annotation of enzyme sequences in the KEGG genome database, about 58% and 65% of the KEGG annotated enzyme sequences have an accurate annotation of the full four EC digits and the first three EC digits, respectively

In Figure 6A and B, we have shown that the family-specific sequence identity threshold is applicable for accurate functional transfer by sequence comparison. Based on these results, we have employed the enzyme family-specific sequence identity threshold to validate the annotation of KEGG enzyme sequences with the result shown in Figure 6C. Among 25,326 KEGG enzyme sequences, 24,697 enzyme sequences can find at least one sequence out of the 22,645 selected SWISS-PROT enzyme sequences by running a PSI-BLAST search. Then, by employing the enzyme family-specific sequence identity threshold, 14,813 (58%) and 16,389 (65%) KEGG sequences can be predicted with the full four EC digits and the first three EC digits, respectively. By comparing the predicted function with the KEGG annotation, we can see that the "prediction accuracy" is 100% when the sequence identity between the KEGG sequence and the SWISS-PROT sequence is above 20% (Figure 6C). Therefore, those KEGG sequences can then be merged with SWISS-PROT enzyme sequences to construct a bigger "clean" enzyme family database that can be found on our website†. However, there are also a large number of KEGG sequences with functions unconfirmed at the level of the full four EC digits (42%), or the first three EC digits (35%), by this method. This does not mean that the annotations of those "unconfirmed" KEGG sequences are wrong, but suggests that those annotations need to be confirmed either by experiment or by more sophisticated measures other than only simple sequence comparison.

In Figure 6C, it can be seen that the percentage of transferable sequence pairs is different from that obtained by using the SWISS-PROT enzyme sequences as the test sequences in the jack-knife analysis (Figure 6A and B). For example, for full EC number transfer at 60–70% sequence identity level, the percentage of transferable sequence pairs is 91% and 80% by using the KEGG annotated enzyme sequences and the SWISS-PROT enzyme sequences as the test sequences, respectively; for first three EC digits transfer at the 50–60% sequence identity level, this percentage is 96% and 84% by using the KEGG annotated enzyme sequences and the SWISS-PROT enzyme sequences as the test sequences, respectively. As mentioned above, this percentage could be regarded as the probability of transferring enzyme functions accurately by employing a family-specific identity threshold. Compared with the SWISS-PROT database, the distribution of enzyme sequences in the KEGG database should be closer

to that in real genomes; therefore, it is possible that the results obtained by evaluating KEGG annotated enzyme sequences might reflect the limit of accurate enzyme function transfer to unknown sequences from simple sequence comparison based on our current knowledge.

Discussion and Conclusion

How well is enzyme function conserved?

It has been established that use of a statistical score, such as the BLAST *E*-value is superior to percentage sequence identity in detecting remote homology¹⁵ or structural similarities, by sequence comparison. However, because functional divergence can happen at high levels of sequence identity,^{16–20} where there is no dispute about homology, the statistical score might not be advantageous over percentage sequence identity for functional inference. In fact, as shown in Figure 2, the *E*-value is not a good measure for transferring function, especially when multiple iterations of PSI-BLAST are conducted. On the other hand, because the percentage of sequence identity is simple, quick and widely accepted by the biologist, several groups have examined the extent to which pairwise sequence identity functional similarity can be inferred. Devos,²⁰ Wilson,¹⁸ and Todd¹⁷ conducted an all-against-all pairwise enzyme sequence comparison, and concluded that when the sequence identity is above 40%, above 90% accuracy can be achieved when transferring the full four digits EC number. However, by reducing the database bias with sequence classification, Rost¹⁹ discovered that the enzyme function conservation is much lower than previously anticipated. He showed that less than 30% of all the pairs found at 50% sequence identity had identical EC numbers, and when the sequence identity is below 70%, the conservation of both the first EC number and the full EC number starts to be below 90%. This is significantly different from other groups' results.

By employing the global identity and running a simple all-against-all pairwise sequence comparison, here we have demonstrated that the conservation of the full EC number and the first three digits of the EC number can be above 90% when the global identity is above 40% and 30%, respectively, which is in agreement with Todd's observation.¹⁷ However, after classifying enzyme sequences by both functional and sequence similarity and averaging the extent of function conservation across all enzyme families, we have confirmed Rost's conclusion that enzyme function conservation is lower than previously anticipated. However, our results also differ from Rost's conclusion in that we find that the degree of enzyme function conservation is not as poor as what he observed. Even in the presence of non-enzymes in the comparison, although transferring all four EC

digits with above 90% accuracy requires above 60% global sequence identity, 40% global sequence identity can still be used to transfer the first three digits of an EC number with above 90% accuracy (Figure 1). Although function conservation varies among different enzyme families, these obtained thresholds of enzyme function conservation are stable and do not differ by the selection of enzyme families (Figure 3).

The effects of the definition of sequence identity on the results of enzyme function conservation

We noticed that employing different definitions of sequence identity leads to different results for enzyme function conservation. Among the five definitions of sequence identity, we found that the global identity has the strongest correlation to function conservation, while the correlation of the aligned sequence identity of the MM alignment and PSI-BLAST sequence identity to enzyme function conservation is worse than the other three definitions of sequence identity we examined (Figure 2). The reasons why the aligned sequence identity and the PSI-BLAST sequence identity has worse correlation to functional conservation can be that the length of the aligned residues in the MM alignment, or the length of the PSI-BLAST alignment might be very short; however, the corresponding sequence identity is high. For example, using PSI-BLAST to search with sequence DEOB_BUCAI (E.C.5.4.2.7, phosphopentomutase) finds the sequence PPB4_BACSU (E.C.3.1.3.1, alkaline phosphatase) with an *E*-value of 3.4, which produces a PSI-BLAST alignment with 19 residues and a reported sequence identity of 63%. In contrast, the global identity of the MM alignment between these two sequences is 14%. Thus, the presence of short alignments with high sequence identity contaminates the pool of sequence pairs having high sequence identity, and makes the extent of function conservation worse than using the global identity. On the other hand, although the aligned region in the MM alignment or the PSI-BLAST alignment might have reasonable length, it might not represent the functional region of the enzyme, or just part of the functional region. For example, the MM alignment between the sequence FENR_SYN3 (E.C.1.18.1.2, ferredoxin-NADP(+) reductase, 413 residues) and the sequence PYS1_SYNEL (non-enzyme, phycobilisome 8.9 kDa linker polypeptide, 77 residues) has an aligned identity of 61%, with a reasonably long aligned region of 74 residues. However, because PYS1_SYNEL does not have any enzymatic activity, but is just a structural protein, the aligned region between these two proteins cannot be the functional domain of FENR_SYN3, but might be a common structural domain for both proteins. Another example, the MM alignment between the sequence THER_BACTH (E.C.3.4.24.27, thermolysin, 316 residues) and the sequence NPPE_PAEPO

(E.C.3.4.24.28, bacillolysin, 517 residues) has an aligned identity of 67%, with 310 aligned residues. However, although their aligned identity is high, because these two proteins have different substrate specificities, the substrate specificity of NPPE_PAEPO might not only be determined by this aligned region, but also by the other parts of the sequence. Overall, for complete transfer of functions between two sequences, the global identity is more accurate, especially when the function of the aligned domain between two proteins is unknown.

Why is enzyme function conservation obtained from our analysis different from Rost's results?

First, we employ the global identity to evaluate the extent of enzyme function conservation, while Rost used the identity derived from the BLAST alignment, a gapped-local alignment. As discussed above, the PSI-BLAST identity is worse for determining the extent of function conservation (Figure 1).

Second, we conduct both functional and sequence similarity classification, while Rost only did sequence similarity classification, which can result in distant homologs with different EC numbers being grouped into the same family. Thus, the selection of the representative sequences after family classification in his procedure may result in missing some enzyme functions in the constructed "unbiased" dataset. In our studies, all types of enzyme functions are compared to derive the level of enzyme function conservation.

Third, Rost employed the pairwise BLAST algorithm to compare each of 1973 sequences in the constructed unbiased dataset with all the original 26,342 sequences that are used to construct the unbiased dataset. Obviously, for each of 1973 sequences, the majority of the 26,342 sequences are unrelated and have no sequence similarity. However, for some of those unrelated sequences, the pairwise BLAST algorithm may generate very short alignments with high sequence identity, which can contaminate the pool of related sequence pairs having high sequence identity and with reasonable alignment length; thus, it can worsen the results of function conservation. Moreover, in Rost's studies, because the original dataset has a bias in the distribution of enzymes, this might still have some effects on the results of enzyme function conservation. For example, the large number of sequences from some functional diverse families might dilute the contribution of those enzymes with a small number of sequences but well conserved functions. In contrast, in our analysis, we calculate the function conservation of each enzyme family and then average the enzyme function conservation across all the enzyme families. This can guarantee that all types of enzyme functions contribute evenly to the final results.

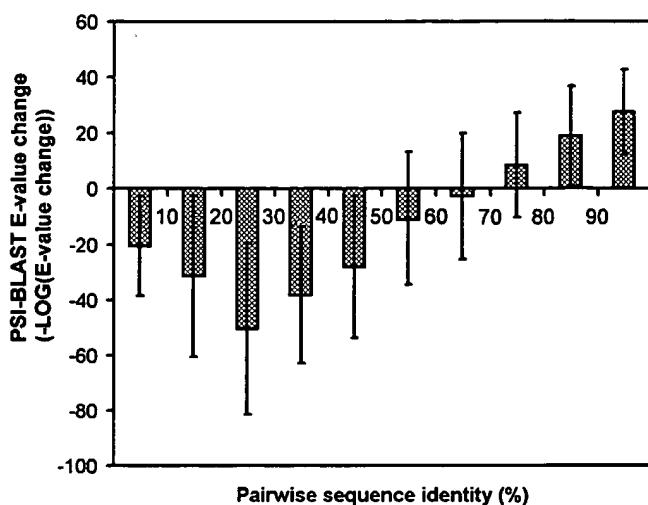


Figure 7. The effects of PSI-BLAST iteration on the PSI-BLAST E-value. The change of PSI-BLAST E-value is shown according to different levels of the global sequence identity.

The effects of PSI-BLAST iteration on transferring of enzyme functions

Our analysis suggests that the *E*-value tends to have a weaker correlation to enzyme function conservation during the iteration process of PSI-BLAST (Figure 2). To understand the reason, we track the change of a hit sequence's *E*-value from the first round to the third round of the PSI-BLAST search. Because the MM alignment between the query sequence and the hit sequence is stable and independent of the iteration process, in Figure 5, we examined the *E*-value changes in terms of the global sequence identity. It is surprising that the *E*-value changes significantly during the iteration process (Figure 7). For a hit sequence with high global identity to a query sequence (above 70%), the *E*-value increases during the iteration of PSI-BLAST search; the average increase of the *E*-value is e^{28} for sequences above 90% sequence identity to the query sequence. However, for hit sequences with low global identity to the query sequence, the *E*-value decreases significantly during the iteration; the average decrease of the *E*-value is even e^{-50} for sequence with 20–30% global identity to the query sequence, i.e. when the *E*-value of a hit sequence is 1 at the first iteration, it could be e^{-50} at the third iteration. A hit sequence with e^{-50} would usually be regarded as significant. However, because of their low global identity, their function might be very different. For example, the sequences of GOX_ASPNG (E.C.1.1.3.4, glucose oxidase) and MDL2_PRUSE (E.C.4.1.2.10, mandelonitrile lyase) have a global identity of around 23%. The PSI-BLAST search with GOX_ASPNG against the SWISSPROT + TREMBL + PDB database hits MDL2_PRUSE with an *E*-value of e^{-10} in the first round, and in the third round of the PSI-BLAST search, the *E*-value of MDL2_PRUSE becomes e^{-115} , which would be thought to be very significant. However, apparently, they do not have similar functions. Probably,

the structure similarity, or evolutionary relationship between distant homologs is detected during the iterations of the PSI-BLAST search, while the functional similarity might not be directly inferred from the *E*-value when multiple iterations of PSI-BLAST search are conducted. This suggests that using the *E*-value from PSI-BLAST to infer functional similarity should be used with caution.

The application of enzyme function conservation for functional inference of unknown sequences by sequence comparison

The main goal of studying enzyme function conservation is to explore the relationship between sequence divergence and functional divergence and derive the threshold of functional inference of unknown sequences. However, because enzyme sequences in fact only account for around 20% of the total number of protein sequences in a genome, the relationship between sequence and enzyme function might not be applicable to other protein functions, such as structural proteins. Thus, the results of enzyme function conservation may only be used for enzyme-related functional inference, i.e. the functional inference when the known sequence is an enzyme. Generally, we would like to know to what extent of pairwise sequence identity could the function of an unknown sequence be transferred from an enzyme. As we have shown in Figure 1, to transfer all four digits and the first three digits of an EC number to an unknown sequence with 90% confidence, above 60% and 40% global sequence identity is required.

However, because functional conservation varies among different enzyme families, rather than using a general threshold of enzyme function conservation for functional inference, we can also take advantage of the information of individual enzyme family to which the known sequence belongs, and develop a family-specific threshold. With a jackknife analysis, we have shown that the prediction

accuracy is almost always 100% and not affected by the level of sequence identity as long as it is above the family-specific threshold (see Figure 6A and B). However, because 100% conservation rate is required for establishing the threshold, this comes at a cost: those true positive sequences below this threshold cannot be uniquely identified. It is possible that more functional inference can be made if we lower the conservation rate to establish the family-specific sequence identity threshold, e.g. using 90% instead of a 100% conservation rate. However, as we have shown in Figure 4E, when the conservation rate of an individual enzyme family is not 100%, it is quite sensitive to the particular set of sequences chosen, suggesting that a substantial number of misannotations could occur if we were to loosen the criteria below 100% accuracy. Considering the big concerns about the pollution of current database by easily spread functional annotation errors,^{13,16-20} it is better to have a smaller number of safe annotations than a larger number of unsure annotations.

For functional inference of those missed true positives that cannot be identified by simple sequence comparison, more sophisticated computational techniques need to be developed, such as constructing multiple sequence alignment to identify signatures that might be associated with functional information or integrating protein structural features.⁴⁰⁻⁴⁵ However, the quality of the functional signature relies on the quality (accurate annotation) and quantity (number) of the sequences in the family. Therefore, we have applied the family-specific sequence identity threshold on KEGG annotated enzyme sequences to expand the original SWISSPROT enzyme database. We have confirmed the function of about 58% and 65% out of 25,326 KEGG enzyme sequences at the level of full EC number and the first three EC numbers, respectively, which together with the original SWISSPROT enzyme sequences can greatly facilitate the accurate functional inference of those missed true positive sequences by more sophisticated measures. A list of those sequences can be found on our website†.

Enzyme functions that are indistinguishable by sequence comparison at a high level of sequence identity

As shown in Figure 5, for enzyme–enzyme only comparisons, 90% of the classified full EC number enzyme families are absolutely conserved when the global sequence identity is above 60%. To understand more about those 10% errant enzyme families, we have listed in the Appendix all enzyme functions that are indistinguishable from each other by sequence comparison with a 60% global pairwise sequence identity cutoff. For a

complete list of combinations of enzyme functions that are indistinguishable from each other at lower global sequence identity, see our website.

Above 60% global sequence identity, there are only a few enzyme functions indistinguishable from each other at the first digit of the EC number: EC 2.4.1.10–EC 3.2.1.26, EC 2.4.1.19–EC 3.2.1.1, EC 2.4.1.25–EC 3.2.1.1, and EC 2.4.1.119–EC 5.3.4.1, respectively (see Appendix). From the point of view of reaction type, these enzyme functions are very different: EC 2.4.1.10 (levansucrase), EC 2.4.1.19 (cyclomaltodextrin glucanotransferase), EC 2.4.1.25 (4- α -glucanotransferase) and EC 2.4.1.119 (dolichyl-diphosphooligosaccharide–protein glycosyltransferase) are all responsible for “hexosyl group transfer”; EC 3.2.1.26 (β -fructofuranosidase) and EC 3.2.1.1 (α -amylase) are both responsible for “hydrolysis of O-glycosyl bond”; EC 5.3.4.1 (protein disulfide isomerase) is responsible for “isomerization”. However, if we look at the substrates and products of the reaction that they catalyze, they do have something in common. EC 2.4.1.19 and EC 3.2.1.1 both can function to degrade starch or glycogen,^{46,47} and EC 2.4.1.19 even has an alternative name: *Bacillus macerans* amylase. Similar to EC 2.4.1.19, EC 2.4.1.25 also was reported to play an important role in starch metabolism.⁴⁸ EC 2.4.1.10 and EC 3.2.1.26 both can function on sucrose to produce β -D-fructose and glucose,^{49,50} though β -D-fructose is then transferred to (2,6- β -D-fructosyl) n by EC 2.4.1.10. For EC 2.4.1.119 and EC 5.3.4.1, it seems that these two enzyme functions are very different: EC 2.4.1.119 is a glycosyltransferase, while EC 5.3.4.1 catalyzes the rearrangement of disulfide bonds in proteins. However, EC 5.3.4.1 can also act as a subunit of a triacylglycerol transfer protein, which facilitates the transfer of lipids to newly synthesized core lipoproteins.⁵¹ Thus, because the definition of EC number is arbitrary, the disagreement of EC number might not necessarily be related to functional disagreement. Nevertheless, this indeed adds to the difficulties of functional inference by computational techniques.

The majority of enzyme functions indistinguishable from each other above 60% only differ at the last digit of the EC number; i.e. mainly by the substrate of the reaction they catalyze, such as EC 1.13.11.31 (arachidonate 12-lipoxygenase) and EC 1.13.11.33 (arachidonate 15-lipoxygenase), EC 1.1.1.149 (20- α -hydroxysteroid dehydrogenase) and EC 1.1.1.50 (3- α -hydroxysteroid dehydrogenase (B-specific)), and EC 1.1.1.27 (L-lactate dehydrogenase) and EC 1.1.1.37 (malate dehydrogenase). There are also enzyme functions that differ in the cofactor of the reaction: such as EC 1.1.1.1 (alcohol dehydrogenase) and EC 1.1.1.2 (alcohol dehydrogenase (NAD⁺)), EC 1.2.1.3 (aldehyde dehydrogenase (NAD⁺)) and EC 1.2.1.5 (aldehyde dehydrogenase (NAD(P)⁺)), and EC 1.6.6.1 (nitrate reductase (NADH)) and EC 1.6.6.2 (nitrate reductase (NAD(P)H)). Some enzyme functions differ in the metal that play

† http://bioinformatics.buffalo.edu/resources/enzyme_conservation

an important role in the reaction, such as EC 1.11.1.13 (Mn-dependent peroxidase) and EC 1.11.1.7 (peroxidase).

All these facts taken together make function annotation complicated when employing computational approaches. As a result, for some particular type of enzyme sequences, experimental approaches are essential to further clarify their functions. On the other hand, other than simple sequence comparison, more sophisticated computation approaches, such as constructing a phylogenetic tree to highlight those residues that are associated with specific protein functions or careful examination of protein structural features, such as active-site residue clusters or characteristic surface properties, might be necessary.⁴⁰⁻⁴⁵

Conclusions

Here, we have classified enzyme families based on both function and sequence similarities and studied the conservation of enzyme function by averaging the function conservation across all the enzyme families. Our results suggest that for function annotation on genome sequences, a 40% sequence identity can still be used as a confident threshold to transfer the first three digits of the EC number; however, to transfer all four digits of an EC number, above 60% sequence identity is needed to have above 90% accuracy. Compared with sequence identity, the weak correlation of *E*-value at the third iteration of PSI-BLAST suggests that functional annotation based on *E*-value should be done with particular caution. By using enzyme family-specific sequence identity thresholds above which 100% conservation rate is required, it is possible to transfer functions accurately. We have applied the enzyme family-specific sequence identity threshold to the KEGG annotated enzyme sequences and about 58% and 65% of the KEGG enzyme sequences have been confirmed at the full EC number and the first three EC number level, respectively.

Methods

Collection of enzyme sequences

Following the strategy employed by Rost to collect enzyme sequences, we retrieved 33,024 sequences that have annotated EC numbers in the "DE" line of the newest version of the SWISSPROT database-sprot40.dat.³⁰ Then, we removed those sequences that: (1) contain EC numbers with undetermined digits (-); (2) have more than one EC number; (3) have keywords with "probable", "hypothetical", "putative", "by homology", or "by similarity"; (4) have the keyword "fragment".

These criteria remove 10,379 sequences and result in a set of 22,645 sequences that will be subject to further classification and which correspond to 1549 different EC numbers. The 22,645 enzyme sequences are strongly dominated by a few enzymes. For example, the three

biggest enzyme groups, EC 1.6.5.3 (NADH dehydrogenase (ubiquinone)), EC 1.9.3.1 (cytochrome *c* oxidase), and EC 3.6.1.34 (H⁺-transporting ATP synthase), have 956, 520, and 1122 sequences, respectively. Together, these three enzyme groups account for 11% of the entire number of enzyme sequences in the SWISSPROT database. However, 70% of the total EC numbers have less than ten sequences each, and together they only account for 17% of the total number of enzyme sequences in the SWISSPROT database. Consequently, the results of enzyme function conservation from a simple all-against-all pairwise sequence comparison based on the current database might be misleading.

Measurements of sequence similarity

The most widely used way to measure sequence similarity between two proteins is their sequence identity. We use two different alignment schemes to obtain sequence identity: (1) the global alignment; and (2) the PSI-BLAST alignment. The global pairwise sequence alignment is conducted by align0, a program that employs the Myers/Miller (MM) global alignment algorithm,⁵² without penalizing for end-gaps. The PSI-BLAST alignment is a gapped-local alignment,¹⁰ which is generated automatically between the query sequence and the hit sequence after a PSI-BLAST search. Because the definition of sequence identity is arbitrary, for global alignment, we explore four definitions of sequence identity: the percentage of identical residues between two proteins in terms of (1) the alignment length (including gaps), the global identity, (2) the length of the protein with the greater number of residues, the big identity, (3) the length of the protein with the smaller number of residues, the small identity, and (4) the length of aligned residues (not counting gaps), the aligned identity.¹⁹ The PSI-BLAST sequence identity is simply adapted from its output, which is calculated by the percentage of identical residues between two proteins in terms of the length of the gapped-local alignment. In all cases, the sequence identity is the ratio of the number of identical aligned residues divided by the total number of residues given by one of the above definitions.

As a second means of purely sequence-based family classification, we also employ the statistical significant score (*E*-value) given by PSI-BLAST as a measure of sequence similarity.

Enzyme family classification

We define an enzyme family as a family of evolutionarily related sequences whose function is conserved. Based on this definition, we first conduct functional classification, by collecting enzyme sequences into groups according to different levels of enzyme function, i.e. the full four digits or the first three digits of their EC number. Then, we conduct a sequence similarity classification within each functional group. For sequence similarity classification, we calculate the HSSP-distance of all sequence pairs within each functional group with the HSSP-threshold *J* set to be -2¹⁰. Then, we conduct a complete linkage analysis to cluster enzyme sequences into families by requiring that the HSSP-distance of all sequence pairs in the family must be larger than 0. Following this strategy, we have classified the selected 22,645 SWISSPROT enzyme sequences into 2431 and 1794 families, with full four digits EC number and the first three digits EC number, respectively.

Typically, enzymes that catalyze the same reaction often show significant sequence and structural similarity; However, although they have the identical EC number, some enzymes may have evolved independently of one another and have different catalytic mechanisms and little structure similarity.⁵³⁻⁵⁵ As a result, for a particular enzyme function, there might be more than one family. For example, there are three families associated with EC 1.1.1.1 (alcohol dehydrogenase), which correspond to three Pfam families: Adh_short, Fe_ADH and Adh_zinc,²⁷ respectively. By running protein structure prediction with threading, these three families hit three different protein structure templates that have no sequence similarity to each other (our unpublished data).

Evaluation of enzyme function conservation

After enzyme family classification, we need to calculate the extent of sequence and function conservation of each enzyme family. To do this, we first collect a list of sequence pairs between sequences from the enzyme family and all the other SWISSPROT enzyme sequences (excluding those removed enzyme sequences) at a certain level of sequence identity, e.g. 40–50% global identity. Then, we compare the functional match of each sequence pair to determine how many of the collected sequence pairs at a particular level of sequence identity are from the same enzyme family:

$$\begin{aligned} & \text{"degree of enzyme family function conservation} \\ & = (\text{number of pairs with same function})/ \\ & (\text{number of all pairs}) \end{aligned}$$

Then, we average the enzyme function conservation across all the enzyme families to obtain the average degree of enzyme function conservation by:

$$\begin{aligned} & \text{"average degree of enzyme function conservation} \\ & = (\sum \text{degree of enzyme family function conservation})/ \\ & (\text{number of enzyme families at that level} \\ & \text{of sequence identity}) \end{aligned}$$

In practice, it is computationally expensive to compare each enzyme sequence with all the other 22,645 enzyme sequences by the MM algorithm. On the other hand, this is also unnecessary. For standard procedure of functional annotation of unknown sequences, usually the first step is a database search, such as PSI-BLAST, to collect possible homologous sequences. Then functional inference from homology is made if possible. Apparently, for each enzyme sequence, only a few out of the 22,645 enzyme sequences can be picked up by PSI-BLAST search and only these sequences are really what we need to pay attention to. Therefore, for each enzyme sequence, we run a PSI-BLAST search against the SWISSPROT + TREMBL + PDB database (over 820,000 sequences in total) with three iterations and pick up only those SWISSPROT sequences (excluding those removed enzyme sequences) with an *E*-value less than 10 for comparison with the query enzyme sequence by the MM algorithm. During the iteration process of PSI-BLAST search, to avoid results drifting from the inclusion of false positive sequences, we set the iteration parameter (*H*-value) to be e^{-10} , the same parameter used by Rost.¹⁹ The hit SWISSPROT sequences can have any function: either an enzyme that belongs to the selected

22,645 SWISSPROT sequences, or a non-enzyme that has no "EC" identifier in the SWISSPROT functional annotation. Thus, after the PSI-BLAST search, for each enzyme family, we obtain two pools of sequence pairs: one that includes only enzyme–enzyme pairs, and the other that includes not only enzyme–enzyme but also enzyme–non-enzyme pairs. These two pools of sequence pairs correspond to two degrees of enzyme function conservation, with the results from comparisons of both enzyme–enzyme and enzyme–non-enzyme pairs representing a more realistic situation when functional transfer is to be assessed.

Bootstrap analysis to assess the stability of the threshold of enzyme function conservation

To assess whether the average enzyme function conservation differs by the selection of enzyme families, we conduct a bootstrap analysis. We randomly choose a subset of enzyme families, ranging from 10%, 20%,...to 90% of the total number of enzyme families with full four EC digits and the first three EC digits, respectively. Then we calculate the degree of enzyme function conservation by averaging the conservation rate across all enzyme families of each subset. This procedure is repeated 100 times. Then for each subset, the variation of function conservation at different level of sequence identity is calculated by:

$$\begin{aligned} & \text{"conservation variation} \\ & = \text{the maximum conservation rate} \\ & - \text{the minimum conservatorium rate"} \end{aligned}$$

Bootstrap analysis to assess the stability of the conservation rate of individual enzyme families

To evaluate whether the conservation rate of individual enzyme families differs by the selection of enzyme sequences, we select those full EC number enzyme families that have more than 30 sequences each (167 enzyme families in total). For each enzyme family, we randomly choose a subset of enzyme sequences, ranging from 10%, 20%,...to 90% of the total, and calculate its function conservation rate. This procedure is repeated 100 times. Then, for each enzyme family's subset, we obtain a conservation variation at different levels of sequence identity, by:

$$\begin{aligned} & \text{"conservation variation} \\ & = \text{the maximum conservation rate} \\ & - \text{the minimum conservatorium rate"} \end{aligned}$$

which is averaged across all enzyme families.

To study whether the conservation variation of individual enzyme families is affected by its conservation rate, we pick up two sets of enzyme families: one is composed of enzyme families that are absolutely conserved above 40% (137 enzyme families in total); another is composed of enzyme families that are absolutely conserved above 50% but not above 40% sequence identity (12 enzyme families in total). Then, following the above procedures, we calculate the average conservation variation with respect to individual enzyme family by using different subsets of enzyme sequences at different sequence identity levels.

Jack-knife analysis to test the usefulness of enzyme family-specific sequence identity threshold in functional inference

The enzyme family-specific sequence identity threshold is defined as the sequence identity above which the conservation rate is 100% and also at which a conservation rate is available. For example, an enzyme family might have a conservation rate of 100% and 50% at 60–70% and 30–40% sequence identity level, respectively, and no conservation rate available at any other sequence identity levels. Then the family-specific sequence identity threshold is 60%. Here, the conservation rates are obtained when both enzyme–enzyme and enzyme–non-enzyme are included in the calculation. To apply this threshold for functional inference, we calculate the global sequence identity between the “unknown” and “known” enzyme sequence. If it is bigger than the threshold of the enzyme family to which the known sequence belongs, then the function of the known sequence is transferred to the unknown sequence. Otherwise, no function is transferred.

To validate this procedure, we conduct a jack-knife analysis. From the original 22,645 SWISSPROT enzyme sequences, we randomly choose a subset of 60%, 70%, 80% and 90% of the total number of enzyme sequences as the training set with the remaining 40%, 30%, 20% and 10%, respectively of the total number of enzyme sequences as the test set, respectively. From each training set, we conduct enzyme family classification and calculate the conservation rate of each enzyme family to derive the family-specific sequence identity threshold. Then, for each test sequence, we run a PSI-BLAST search against the SWISSPROT + TREMBLE + PDB database with three iterations to pick up the functionally known training sequences. After PSI-BLAST search of all test sequences, we pool the test-training sequence pairs together according to different level of sequence identity. For each test-training sequence pair, we attempt the functional inference of the test sequence by applying the family-specific sequence identity threshold of the training sequence. If function can be transferred, this sequence pair is called transferable. If the sequence pair is non-transferable, however, the test and training sequence do have the same function, it is called missed. Then, at different levels of global sequence identity, we calculate:

$$\begin{aligned} & \text{“percentage of transferable sequence pairs} \\ & = (\text{number of transferable sequence pairs}) / \\ & (\text{number of all sequence pairs}) \end{aligned}$$

$$\begin{aligned} & \text{“prediction accuracy} = (\text{number of transferable} \\ & \text{sequence pairs with right prediction}) / \\ & (\text{number of transferable sequence pairs}) \end{aligned}$$

and:

$$\begin{aligned} & \text{“percentage of missed sequence pairs} \\ & = (\text{number of missed sequence pairs}) / \\ & (\text{number of all sequence pairs with same function}) \end{aligned}$$

For example, for one subset with 70% of the total number of enzyme sequences as the training set and the

remaining 30% sequences as the test set, at 30–40% sequence identity level, we collect 45,362 test-training sequences pairs in total. Among those sequence pairs, functional inference can be done at the level of the full four EC numbers for 23,165 sequence pairs (transferable) and they all have right predictions. However, there are actually 39,001 sequence pairs with same function. In other words, 15,836 sequence pairs are missed. Thus, the percentage of transferable sequence pairs, the prediction accuracy, and the percentage of missed sequence pairs at 30–40% sequence identity level are 51%, 100%, and 41%, respectively. This procedure is repeated 100 times to obtain the average of the three percentages at different levels of sequence identity.

The application of the enzyme family-specific sequence identity threshold to evaluate the annotation of KEGG enzyme sequences

The Kyoto Encyclopedia of Genes and Genomes (KEGG) is a database for systematic analysis of gene functions in terms of the networks of genes and molecules, i.e. pathways including both metabolic pathways and regulatory pathways.³⁶ For each metabolic pathway, KEGG has a reference pathway including all possible enzymatic reactions and also a number of organism-specific reconstructed pathways composed of annotated enzymes in each corresponding genome. However, sequence comparison is the main annotation method used by KEGG. To evaluate the annotation of KEGG sequences, we have selected 25,326 KEGG sequences that have been annotated with a unique EC number by KEGG and are not identical with any enzyme sequences in the SWISSPROT database. Then the function of those 25,326 KEGG sequences is predicted by employing the enzyme family-specific sequence identity threshold calculated from the 22,645 SWISSPROT enzyme sequences. After prediction, we calculate the percentage of transferable sequence pairs and the prediction accuracy at different level of global sequence identity. The prediction accuracy is calculated by comparing the KEGG annotation with the predicted function.

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Appendix A

Table A1. Enzyme functions indistinguishable from each other by sequence identity (above 60% global identity)

Enzyme 1	Enzyme 2	Example gene of enzyme 1	Example gene of enzyme 2	ID (%)
<i>Global sequence identity 90–100%</i>				
1.13.11.31 (Arachidonate 12-lipoxygenase)	1.13.11.33 (Arachidonate 15-lipoxygenase)	LOX2_RABIT	LOX1_RABIT	99
2.4.1.19 (Cyclomaltodextrin glucanotransferase)	3.2.1.1 (α-Amylase)	CDGU_BACCI	AMYR_BACS8	97
3.1.3.6 (3'-nucleotidase)	3.1.4.21 (Aspergillus nuclease S ₁)	NUP3_PENSQ	NUP1_PENCI	99
3.4.21.35 (Tissue kallikrein)	3.4.21.77 (Semenogelase)	KLK3_MACMU	KLK3_HUMAN	90
<i>Global sequence identity 80–90%</i>				
1.11.1.13 (Mn-dependent peroxidase)	1.11.1.7 (Peroxidase)	PEM4_PHACH	PEM1_PHACH	83
1.13.11.31 (Arachidonate 12-lipoxygenase)	1.13.11.33 (Arachidonate 15-lipoxygenase)	LOX2_BOVIN	LOX1_HUMAN	86
1.14.13.30 (Leukotriene-B ₄ 20-monoxygenase)	1.14.99.8 (Unspecific monooxygenase)	CPF2_HUMAN	CPF8_HUMAN	81
1.14.14.1 (Unspecific monooxygenase)	1.14.15.3 (Alkane-1 monooxygenase)	CP44_RABIT	CP45_RABIT	86
2.4.1.119 (Dolichyl-diphosphooligosaccharide-protein glycosyltransferase)	5.3.4.1 (Protein disulfide isomerase)	GSBP_CHICK	PDI_BOVIN	83
2.4.1.19 (Cyclomaltodextrin glucanotransferase)	3.2.1.1 (α-Amylase)	CDGT_BACS0	AMYR_BACS8	86
2.4.1.203 (Zeatin O-β-D-glucosyltransferase)	2.4.1.204 (Zeatin O-β-D-xylosyltransferase)	ZOG_PHALU	ZOX_PHAU	85
3.4.21.35 (Tissue kallikrein)	3.4.21.54 (Gamma-renin)	KLK8_MOUSE	KLKG_MOUSE	80
3.4.22.15 (Cathepsin L)	3.4.22.43 (Cathepsin V)	CATL_PIG	CSL2_HUMAN	80
3.4.22.25 (Glycyl endopeptidase)	3.4.22.30 (Caricain)	PAP4_CARPA	PAP3_CARPA	80
3.4.24.27 (Thermolysin)	3.4.24.28 (Bacillolysin)	THEB_BACST	NPRE_BACCL	85
3.4.24.42 (Atrypsin C)	3.4.24.46 (Adamalysin)	HRT2_CRORU	ADAM_CROAD	80
<i>Global sequence identity 70–80%</i>				
1.1.1.188 (Prostaglandin-F synthase)	1.3.1.20 (<i>trans</i> -1,2-Dihydrobenzene-1,2-diol dehydrogenase)	PGF2_BOVIN	DBDD_HUMAN	77
1.13.11.31 (Arachidonate 12-lipoxygenase)	1.13.11.33 (Arachidonate 15-lipoxygenase)	LOX2_RAT	LOX1_HUMAN	74
1.14.13.30 (Leukotriene-B ₄ 20-monoxygenase)	1.14.99.8 (Unspecific monooxygenase)	CPF2_HUMAN	CPF1_RAT	78
1.14.14.1 (Unspecific monooxygenase)	1.14.15.3 (Alkane-1 monooxygenase)	CP44_RABIT	CP41_RAT	73
1.2.1.12 (Glyceraldehyde 3-phosphate dehydrogenase (phosphorylating))	1.2.1.59 (Glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) (phosphorylating))	G3P2_ANASQ	G3P2_SYN3	74

(continued)

Table A1 continued

Enzyme 1	Enzyme 2	Example gene of enzyme 1	Example gene of enzyme 2	ID (%)
1.4.1.2 (Glutamate dehydrogenase)	1.4.1.4 (Glutamate dehydrogenase (NADP ⁺))	DHE2_PORGI	DHE4_BACFR	72
1.6.6.1 (Nitrate reductase (NADH))	1.6.6.2 (Nitrate reductase (NAD(P)H))	NIA1_ARATH	NIA_BETVE	72
2.3.1.74 (Naringenin-chalcone synthase)	2.3.1.95 (Trihydroxystilbene synthase)	CHS1_CAMSI	THS1_ARAHY	74
2.4.1.119 (Dolichyl-diphosphooligosaccharide-protein glycosyltransferase)	5.3.4.1 (Protein disulfide isomerase)	GSBP_CHICK	PDI_CHICK	73
2.4.1.19 (Cyclomaltodextrin glucanotransferase)	3.2.1.1 (α-Amylase)	CDGT_BACCI	AMYR_BACS8	71
2.4.1.25 (4-α-Glucanotransferase)	3.2.1.1 (α-Amylase)	MALQ_PYRKO	AMYA_PYRAB	71
3.2.1.39 (Glucan <i>endo</i> -1,3-β-D-glucosidase)	3.2.1.73 (Licheninase)	E132_SOLTU	GUB_NICPL	70
3.2.1.8 (<i>endo</i> -1,4-β-Xylanase)	3.2.1.91 (Cellulose 1,4-beta-cellobiosidase)	XYNA_THESA	XYNX_CLOTM	75
3.4.21.35 (Tissue kallikrein)	3.4.21.54 (Gamma-renin)	KLK1_MOUSE	KLKG_MOUSE	69
3.4.21.35 (Tissue kallikrein)	3.4.21.77 (Semenogelase)	KLK2_HUMAN	KLK3_HUMAN	77
3.4.22.15 (Cathepsin L)	3.4.22.43 (Cathepsin V)	CATL_BOVIN	CSL2_HUMAN	78
3.4.22.2 (Papain)	3.4.22.30 (Caricain)	PAPA_CARPA	PAP3_CARPA	72
3.4.24.17 (Stromelysin 1)	3.4.24.22 (Stromelysin 2)	MM03_HORSE	MM10_HUMAN	74
3.4.24.27 (Thermolysin)	3.4.24.28 (Bacillolysin)	THE_BACST	NPRS_BACST	70
3.5.1.1 (Asparaginase)	3.5.1.38 (Glutaminase-(asparagin-)ase)	ASPC_PSEFL	ASPO_PSE7	79
3.6.1.34 (H ⁺ -transporting two-sector ATPase)	3.6.3.15 (Sodium-transporting two-sector ATPase)	ATPB_ANASP	ATPB_PROMO	70
<i>Global sequence identity 60–70%</i>				
1.1.1.1 (Alcohol dehydrogenase)	1.1.1.2 (Alcohol dehydrogenase (NADP ⁺))	ADH1_ALLMI	ADH4_RANPE	62
1.1.1.149 (20-α-Hydroxysteroid dehydrogenase)	1.1.1.188 (Prostaglandin-F synthase)	PE2R_RAT	PGF2_BOVIN	67
1.1.1.149 (20-α-Hydroxysteroid dehydrogenase)	1.1.1.50 (3-α-Hydroxysteroid dehydrogenase (B-specific))	PE2R_RAT	DIDH_RAT	67
1.1.1.149 (20-α-Hydroxysteroid dehydrogenase)	1.3.1.20 (<i>trans</i> -1,2-Dihydrobenzene-1,2-diol dehydrogenase)	PE2R_RAT	DBDD_HUMAN	68
1.1.1.188 (Prostaglandin-F synthase)	1.1.1.50 (3-α-Hydroxysteroid dehydrogenase (B-specific))	PGF2_BOVIN	DIDH_RAT	69
1.1.1.206 (Tropine dehydrogenase)	1.1.1.236 (Tropine reductase)	TRN1_DATST	TRN2_DATST	61
1.1.1.27 (L-lactate dehydrogenase)	1.1.1.37 (Malate dehydrogenase)	LDH_BOTBR	MDH_RHILV	68
1.1.1.50 (3-α-Hydroxysteroid dehydrogenase (B-specific))	1.3.1.20 (<i>trans</i> -1,2-Dihydrobenzene-1,2-diol dehydrogenase)	DIDH_RAT	DBDD_HUMAN	69
1.13.11.31 (Arachidonate 12-lipoxygenase)	1.13.11.33 (Arachidonate 15-lipoxygenase)	LOXE_MOUSE	LOX1_HUMAN	66
1.14.14.1 (Unspecific monooxygenase)	1.14.15.3 (Alkane-1 monooxygenase)	CP48_RAT	CP42_RAT	69
1.2.1.12 (Glyceraldehyde 3-phosphate dehydrogenase (phosphorylating))	1.2.1.59 (Glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) (phosphorylating))	G3PA_ARATH	G3P2_SYN3	60
1.2.1.22 (Lactaldehyde dehydrogenase)	1.1.1.70 (Aldehyde dehydrogenase (NAD ⁺))	ALDB_ECOLI	DHA2_ALCEU	68
1.2.1.3 (Aldehyde dehydrogenase (NAD ⁺))	1.2.1.5 (Aldehyde dehydrogenase (NAD(P) ⁺))	DHA1_BOVIN	DHA6_HUMAN	68
1.3.1.19 (<i>cis</i> -1,2-Dihydrobenzene-1,2-diol dehydrogenase)	1.3.1.56 (<i>cis</i> -2,3-Dihydrobiphenyl-2,3-diol dehydrogenase)	BNZE_PSEPU	BPHB_COMTE	61
1.3.5.1 (Succinate dehydrogenase (ubiquinone))	1.3.99.1 (Succinate dehydrogenase)	DHSB_RECAM	DHSB_RICPR	63
1.3.5.1 (Succinate dehydrogenase (ubiquinone))	1.3.99.1 (Succinate dehydrogenase)	DHSA_DROME	DHSA_RICPR	60
1.5.99.10 (Dimethylamine dehydrogenase)	1.5.99.7 (Trimethylamine dehydrogenase)	DHDM_HYPSX	DHTM_METME	63
1.6.6.1 (Nitrate reductase (NADH))	1.6.6.2 (Nitrate reductase (NAD(P)H))	NIA1_ARATH	NIA7_HORVU	63
2.1.1.53 (Putrescine N-methyltransferase)	2.5.1.16 (Spermidine synthase)	PMT2_TOBAC	SPD1_PEA	61
2.3.1.74 (Naringenin-chalcone synthase)	2.3.1.95 (Trihydroxystilbene synthase)	CHS1_GERHY	THS1_ARAHY	69
2.4.1.10 (Levansucrase)	3.2.1.26 (β-Fructofuranosidase)	SACB_ZYMMO	INVB_ZYMMO	61
2.4.1.19 (Cyclomaltodextrin glucanotransferase)	3.2.1.1 (α-Amylase)	CDG1_PAEMA	AMYR_BACS8	66
2.4.1.25 (4-α-Glucanotransferase)	3.2.1.1 (α-Amylase)	MALQ_PYRKO	AMYA_PYRAB	69
2.7.1.11 (6-phosphofructokinase)	2.7.1.90 (Diphosphate-fructose-6-phosphate 1-phototransferase)	K6P1_STRCO	PFP_AMYME	68
2.7.7.7 (DNA-directed DNA polymerase)	2.7.7.7 (DNA-directed DNA polymerase)	DPOD_PLAFK	DPOD_PLAFK	64
2.8.1.1 (Thiosulfate sulfurtransferase)	2.8.1.2 (3-Mercaptopyruvate sulfurtransferase)	THTR_MOUSE	THTM_RAT	60
3.2.1.1 (α-Amylase)	3.2.1.98 (Glucan 1,4-alpha-maltohexa-oxidase)	AMY_BACAM	AMT6_BACS7	63

(continued)

Table A1 continued

Enzyme 1	Enzyme 2	Example gene of enzyme 1	Example gene of enzyme 2	ID (%)
3.2.1.21 (β -Glucosidase)	3.2.1.86 (6-Phospho-beta-glucosidase)	BGL1_BACSU	ABGA_CLOLO	63
3.2.1.39 (Glucan <i>endo</i> -1,3-beta-D-glucosidase)	3.2.1.73 (Licheninase)	E13B_HEVBR	GUB_NICPL	64
3.4.17.1 (Carboxypeptidase A)	3.4.17.15 (Carboxypeptidase A2)	CBP1_HUMAN	CBP2_RAT	62
3.4.21.1 (Chymotrypsin)	3.4.21.32 (Brachyurin)	CTR1_PENVA	COGS_UCAPU	64
3.4.21.2 (Chymotrypsin C)	3.4.21.71 (Pancreatic elastase II)	CLCR_HUMAN	EL2A_HUMAN	62
3.4.21.35 (Tissue kallikrein)	3.4.21.54 (Gamma-renin)	KLK1_RAT	KLKG_MOUSE	64
3.4.21.35 (Tissue kallikrein)	3.4.21.77 (Semenogelase)	KLK1_HUMAN	KLK3_HUMAN	60
3.4.21.74 (Venombin A)	3.4.21.95 (Snake venom factor V activator)	VSP1_AGKCO	VSPA_DABRU	61
3.4.22.2 (Papain)	3.4.22.25 (Glycyl endopeptidase)	PAPA_CARPA	PAP4_CARPA	68
3.4.22.2 (Papain)	3.4.22.6 (Chymopapain)	PAPA_CARPA	PAP2_CARPA	61
3.4.22.25 (Glycyl endopeptidase)	3.4.22.6 (Chymopapain)	PAP4_CARPA	PAP2_CARPA	67
3.4.22.30 (Caricain)	3.4.22.6 (Chymopapain)	PAP3_CARPA	PAP2_CARPA	65
3.4.23.38 (Plasmeprin I)	3.4.23.39 (Plasmeprin II)	PLM1_PLAFA	PLM2_PLAFA	65
3.4.24.15 (Thimet oligopeptidase)	3.4.24.16 (Neurolysin)	MEPD_HUMAN	NEUL_RABIT	60
3.4.24.17 (Stromelysin 1)	3.4.24.22 (Stromelysin 2)	MM03_HORSE	MM10_MOUSE	68
3.4.24.42 (Atrolysin C)	3.4.24.44 (Atrolysin E)	HRTD_CROAT	HRTE_CROAT	63
3.4.24.53 (Trimerelysin II)	3.4.24.72 (Fibrolase)	HR2_TRIFL	FIBR_AGKCO	61
3.6.1.34 (H(+)-transporting two-sector ATPase)	3.6.3.15 (Sodium-transporting two-sector ATPase)	ATPA_ANASP	ATPA_PROMO	60
3.6.3.10 (Hydrogen/potassium-exchanging ATPase)	3.6.1.37 (Sodium/potassium-exchanging ATPase)	ATHA_CANFA	A1A1_ANGAN	60
4.1.1.25 (Tyrosine decarboxylase)	4.1.1.27 (Aromatic-L-amino-acid decarboxylase)	TYD2_PETCR	TYD1_PAPSO	65
4.2.99.9 (O-succinylhomoserine (thiol)-lyase)	4.4.1.8 (Cystathionine beta-lyase)	METB_HELPJ	METC_LACLA	63
6.2.1.4 (Succinate-CoA ligase (GDP-forming))	6.2.1.5 (Succinate-CoA ligase (ADP-forming))	SUCA_DICDI	SUCD_COXBU	60

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